

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2003, 06:55:31 ; Search time 22 Seconds

(without alignments)
1400.105 Million cell updates/sec

Title: US-09-836-392-21

Perfect score: 3822

Sequence: 1 MRLRLATDAMKMFSEFROE.....IFYQSYELGRLBACTRRKR 728

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/1aa/5A.COMB.rep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.rep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.rep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.rep.*
5: /cgn2_6/ptodata/2/1aa/PTCUTS.COMB.rep.*
6: /cgn2_6/ptodata/2/1aa/backfile1.rep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	275.5	7.2	394	US-09-345-473E-19	Sequence 19, Appl
2	244.5	6.4	823	US-09-886-319A-63	Sequence 63, Appl
3	243.5	6.4	505	US-08-222-616-20	Sequence 20, Appl
4	243.5	6.4	505	US-08-446-648-20	Sequence 20, Appl
5	243.5	6.4	505	US-08-492-723-2	Sequence 2, Appl
6	243.5	6.4	505	PCT-US95-04228-20	Sequence 20, Appl
7	243	6.4	455	US-09-221-235-5	Sequence 5, Appl
8	243	6.4	455	US-09-221-928-5	Sequence 5, Appl
9	243	6.4	455	US-09-221-928-5	Sequence 5, Appl
10	243	6.4	455	US-09-221-236-5	Sequence 5, Appl
11	243	6.4	455	US-09-221-416-5	Sequence 5, Appl
12	243	6.4	455	US-09-221-245-5	Sequence 5, Appl
13	243	6.4	455	US-09-163-115-5	Sequence 5, Appl
14	243	6.4	455	US-09-221-528-5	Sequence 5, Appl
15	243	6.4	455	US-09-593-553-5	Sequence 5, Appl
16	243	6.4	455	US-09-221-237-5	Sequence 5, Appl
17	243	6.4	455	US-09-399-588-2	Sequence 2, Appl
18	241.5	6.3	506	US-08-425-509A-6	Sequence 6, Appl
19	241.5	6.3	511	US-08-232-585-6	Sequence 6, Appl
20	241.5	6.3	511	PCT-US95-05008-6	Sequence 6, Appl
21	238	6.2	800	US-08-469-537A-72	Sequence 72, Appl
22	238	6.2	800	US-08-469-537A-72	Sequence 72, Appl
23	236	6.2	937	US-08-469-537A-105	Sequence 105, Appl
24	236	6.2	263	US-09-035-706-5	Sequence 5, Appl
25	236	6.2	263	US-08-955-841-5	Sequence 5, Appl
26	236	6.2	263	US-09-390-425-5	Sequence 5, Appl
27	236	6.2	263	US-09-566-906-5	Sequence 5, Appl

28	236	6.2	821	US-07-928-464-2	Sequence 2, Appl
29	236	6.2	821	US-08-003-311B-2	Sequence 2, Appl
30	236	6.2	821	US-08-261-432-2	Sequence 2, Appl
31	236	6.2	821	PCT-US93-07347-2	Sequence 2, Appl
32	233	6.1	795	US-09-031-563-23	Sequence 23, Appl
33	233	6.1	795	US-09-392-277-23	Sequence 23, Appl
34	233	6.1	795	US-09-258-000-23	Sequence 23, Appl
35	231.5	6.1	822	US-09-886-319A-64	Sequence 64, Appl
36	230	6.0	865	US-09-417-197-111	Sequence 11, App
37	228.5	6.0	579	US-09-529-279-4	Sequence 4, Appl
38	228.5	6.0	579	US-10-158-895-4	Sequence 4, Appl
39	228.5	6.0	590	US-09-529-279-15	Sequence 15, Appl
40	228.5	6.0	590	US-10-158-895-15	Sequence 15, Appl
41	228	6.0	296	US-08-701-191A-29	Sequence 29, Appl
42	228	6.0	668	US-08-205-018A-2	Sequence 2, Appl
43	228	6.0	859	US-08-395-580-2	Sequence 2, Appl
44	228	6.0	859	PCT-US95-02792-2	Sequence 2, Appl
45	224.5	5.9	943	US-08-469-537A-107	Sequence 107, App

ALIGNMENTS

```
RESULT 1
US-09-345-473E-19
Sequence 19, Application US/09345473E
Patent No. 6558903
GENERAL INFORMATION:
APPLICANT: Hodge, Martin
TITLE OF INVENTION: NO. 6558903el Kinases and Uses Thereof
FILE REFERENCE: 35800/185781
CURRENT APPLICATION NUMBER: US/09/345,473E
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 19
LENGTH: 394
TYPE: PRT
ORGANISM: Homo sapiens
US-09-345-473E-19

Query Match
Best Local Similarity 31.3%; Pred. No. 9.2e-18;
Matches 78; Conservative 42; Mismatches 92; Indels 37; Gaps 8;

QY 3 RHRATDAMKMFSEFROEASMLALOHPCIVAGISIH--LCFALDELAPSSANTVL 60
DB 33 RHDPDEDISQTEIENVQEAFLFAMLKHPNIIALRGVCLKEPNLCIWEFARGGPANRVL 92
QY 61 ENADSSFTPIGHMLTQKI---AYQASGLALVHK--NIIFDLKSDNIIWML--- 110
DB 93 -----GKRIPIIIVNMAVOIARGMNVLHDEAIPIIHRDKSNIIILIOKVEN 141
QY 111 -DYKEHINIKLSDYGISRQSFHEGALGVEGTPGYQAPRIPIVDEKYMFSYGVLYE 169
DB 142 GDLSNKKI-LKTTDGLAREHRTTKMSAATYAWAPVIRASMFKSGDWSYGLTWE 200
QY 170 LLSCGPALGHQIQI-----KLSGKIPVIGQPEVQFRRLQILMMECHMDTKREKP 224
DB 201 LLTEVFPFGIDGLRIVGVAMNKLALPISTCEP-----FAKLMDQWNPDSHRP 253
QY 225 LALVSQW 233
DB 254 SFTNIDQL 262

RESULT 2
US-09-886-319A-63
Sequence 63, Application US/09886319A
Patent No. 6586185
GENERAL INFORMATION:
APPLICANT: Wolf, Eckard
APPLICANT: Werner, Sabine
```

APPLICANT: Halle, Jorn-Peter
APPLICANT: Regenbogen, Johannes
APPLICANT: Goppelt, Andreas
TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
TITLE OF INVENTION: Active Substances
FILE REFERENCE: 50125/014002
CURRENT APPLICATION NUMBER: US/09/886,119A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: DE 10030149.5
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 63
LENGTH: 823
TYPE: PRT
ORGANISM: Mus musculus
US-09-886-319A-63

Query Match 6.4%; Score 244.5; DB 4; Length 823;
Best Local Similarity 32.6%; Pred. No. 3e-14;
Matches 77; Conservative 37; Mismatches 85; Indels 37; Gaps 10;

QY 16 EPRQASMLHALQHPCTVALIGISI--HPLCFALSLAPLSSINTVLSERNADSSFIPLGH 73
DB 605 KFLQEKIKLKQYDHPETVLIGCTQROQVYIMELVPGDFLFLRRKDELKCOL-- 662
QY 74 MLTKIAYQIASGLAVLHKNIIFCDLSKNILVSLDVKEHINIKLSDYISROSFTHEG 133
DB 663 ---VRFSLVAAGMLYLESKNCIHRDLAARNCL-----VGENNTLKISDFEMSQ--EDG 712
QY 134 AGVGEFTPG-----YQAPETPRRIYVDEKVMFSYGMVLYELLS--GQRPALGHLOLI 185
DB 713 --GVYSSGLKQIPIKWTAPFALNYGRYSSESDVWSFGILLMETFSLGVCYPGPTNQQA 770
QY 186 AKKLSKGRPVLGQ--PEEVQFRRLQALMMECWDTEKPEKRP-----LALSVASOM 233
DB 771 REQVGRGYMSAPQNCPEEV-----FTIMKCMQDYKPNRKPFDLHKLIVLYIKM 821

RESULT 3

US-08-222-616-20
Sequence 20, Application US/08222616
Patent No. 563177

GENERAL INFORMATION:

APPLICANT: Bennett, Brian D.
APPLICANT: Goedel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patlin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,616
FILING DATE: 4-APR-1994
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00586
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/826935
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 821P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-222-616-20

Query Match 6.4%; Score 243.5; DB 1; Length 505;
Best Local Similarity 30.5%; Pred. No. 1.7e-14;
Matches 75; Conservative 49; Mismatches 77; Indels 45; Gaps 11;

QY 15 SEPRQASMLHALQHPCTVALIGISI--HPLCFALSLAPLSSINTVLSERNADSSFIPLG 72
DB 272 NDLFRAQIMGNLHPKLIQIYAVCTEDPIYITELMRGSIQBYL--QNDTSKI----- 326
QY 73 HMLTKI--AVQIASGLAVLHKNIIFCDLSKNILVSLDVKEHINIKLSDYISR--- 127
DB 327 -HLFQVMAQVAGMALYLESRNYIHRDLAARNVL-----VGEHNIYKVADPGLARVTK 380
QY 128 -----QSFHEGALGVGTPGYAPETPRRIYVDEKVMFSYGMVLYELLS--GQRPALG 179
DB 361 VDNEDIYSRHEIKLPKWT---APPAISNKSFSISDVWSFGILLMETFSLGVCYPGPTNQQA 436
QY 180 HHQLIQAKLSKGRPVLGQPEEVQFRRLQALMMECWDTEKPEKRP-----LALSVASOM 239
DB 437 MTGAQVIGMAQVNR--LPQSNCP--QGFNIMLEGMNAPEKRP-----PTFR 481
QY 240 TFWTEL 245
DB 482 TLRWEL 487

RESULT 4

US-08-446-648-20
Sequence 20, Application US/08446648
Patent No. 631302

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
APPLICANT: Bennett, Brian D.
APPLICANT: Goedel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: winpatlin (Genentech)
CURRENT APPLICATION DATA:

```

NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 8470-121
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acid
TOPOLGY: linear
MOLECULE TYPE: protein
US-08-492-723-2

Query Match      6 4% Score 243.5; DB 4; Length 505;
Best Local Similarity 30.5%; Pred. No. 1.7e-14;
Matches 75; Conservative 49; Mismatches 77; Indels 45; Gaps 11;

QY 15 SEPRBASMLHALQHPCIVALIGISI--HPLCFALBAPASSINTVLSBNARDSSFIPLG 72
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 272 NPLRBAQMKNLRLPHKILQLYAVCTLEDPIYITTELMDHGSLQEYL-QNDTGSKI----- 326
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 73 HNLTKKI-AVQIASGLAYLHKRIITICDLKSNNLLWMLDYKEHNITLSPTYGISR--- 127
   :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 327 -HLTQVDMAAQVASGAVALYESRRYIHRDIAARNVL-----VGENHYKVADFGLARVFK 380
   :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 128 -----SDFEGALGVSGTPGYAPEIRPRIYVDKVMDFSYGMVLYELL-SGORPALG 179
   :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 381 VNEDIYERHHIKLPVKMT----APPAISNKFSTKSDVMSRGILLVIITYGCMPTSG 436
   :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 180 HHQLQAKLSKGIRPVLGQPEEYQFRRLOALMMECWDTRPKRPPLASVSQMKDPFA 239
   :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 437 MTGAQVIVQMLAQNRY--LPQPSNCP-QQFYNIIMLCMAALEPKEK-----PTFE 481
   :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 240 TEMVEL 245
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 482 TLRMKL 487
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 6
PCT-US95-04228-20
Sequence 20, Application PC/TUS9504228
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William F.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
City: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04228
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee

```

REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 821P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US95-04228-20

Query Match 6.4%; Score 243.5; DB 5; Length 505;
Best Local Similarity 27.9%; Pred. No. 1.5e-14;
Matches 75; Conservative 49; Mismatches 77; Indels 45; Gaps 11;

QY 15 SEFRQASMLHAIQHPCIVALLIGISI--HPCFALELAPLSLNTVISENARDSSFIPLG 72
DB 272 NDFLRQAQIMKRIHFKILQYAVCTLEDPYIITELNRHSLQEYL-QNDTGSKI---- 326
QY 73 HMLTKI--AYQIASLAYLHKNIIFCDLSKNILVMSLDVKEHINKLSDYGISR--- 127
DB 327 -HLTQGVMAAQVASSMAYLESBNYIHRDLARNV-----VGEHNTYKVADPGLAVFK 380
QY 128 -----QSFEHGAIGVGTGPGYQAPRIPIVYDEKVMFSYGMVLYELLS--GQRPALG 179
DB 381 VDNEDIYESRHEIKLPVKWT---APEAIRSNKFSIKSDWSFGILYEITITKMPYSG 436
QY 180 HHQLQIAKKLSKIRPVLCQPEEVOFRRLQALMMECWDTPEKRPALSVSQMKDPTFA 239
DB 437 MGAQVYIQMLAQNYR--LPQPSNCP-QCPYNTIMECWAEPKEX-----PTFE 481
QY 240 TFWYEL 245
DB 482 TLRWKL 487

RESULT 7
US-09-221-235-5
Sequence 5, Application US/09221235
Patent No. 6043040
GENERAL INFORMATION:
APPLICANT: Acton, Susan
TITLE OF INVENTION: NOVEL CSAPE-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
FILE REFERENCE: NMI-050
CURRENT APPLICATION NUMBER: US/09/221,235
CURRENT FILING DATE: 1998-12-28
EARLIER APPLICATION NUMBER: 09/163,115
EARLIER FILING DATE:
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 455
TYPE: PRT
ORGANISM: Homo sapiens
US-09-221-235-5

Query Match 6.4%; Score 243; DB 3; Length 455;
Best Local Similarity 27.9%; Pred. No. 1.5e-14;
Matches 69; Conservative 52; Mismatches 100; Indels 26; Gaps 7;

QY 10 AMKNSEFRQASMLHAIQHPCIVALLIGISIHPLCFAL--ELAPLSLNTVISENARDSS 67
DB 43 AVKGLKIKERAEILSVLSHRNIIQFYGVILEPKNYGVITEVASIGSYDYNR--SE 100
QY 68 FPLGMLTQKIAVOIASGLAYLHK--NIIFCDLSKNILVMSLDVKEHINKLSDYG 124
DB 101 EMDMDHIMTW--ATDVAKGMHYLMEAPYKVIHRDLKSRNVIALDGV-----LKICDFG 153
QY 125 ISRQSFHGAIGVGTGPGYQAPRIPIVYDEKVMFSYGMVLYELLSGQRPALGHQLO 184
DB 154 ASRFNHTTMSLVGTGPGYQAPRIPIVYDEKVMFSYGMVLYELLSGQRPALGHQLO 213

QY 185 IAKKLSKIRPVLCQPEEVOF-----RRLQALMMECWDTPEKRPALSVSQMKDPTFA 239
DB 214 VAWL-----VVEKNERLITPSSCPSPFAELHQCWEADAKKPSFKQIISLESMSND 266
QY 240 TFWYELC 246
DB 267 TSLPDKC 273

RESULT 8
US-09-221-928-5
Sequence 5, Application US/09221928
Patent No. 6121030
GENERAL INFORMATION:
APPLICANT: Acton, Susan
TITLE OF INVENTION: NOVEL CSAPE-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
FILE REFERENCE: NMI-050
CURRENT APPLICATION NUMBER: US/09/221,928
CURRENT FILING DATE: 1998-12-28
EARLIER APPLICATION NUMBER: 09/163,115
EARLIER FILING DATE:
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 455
TYPE: PRT
ORGANISM: Homo sapiens
US-09-221-928-5

Query Match 6.4%; Score 243; DB 3; Length 455;
Best Local Similarity 27.9%; Pred. No. 1.5e-14;
Matches 69; Conservative 52; Mismatches 100; Indels 26; Gaps 7;

QY 10 AMKNSEFRQASMLHAIQHPCIVALLIGISIHPLCFAL--ELAPLSLNTVISENARDSS 67
DB 43 AVKGLKIKERAEILSVLSHRNIIQFYGVILEPKNYGVITEVASIGSYDYNR--SE 100
QY 68 FPLGMLTQKIAVOIASGLAYLHK--NIIFCDLSKNILVMSLDVKEHINKLSDYG 124
DB 101 EMDMDHIMTW--ATDVAKGMHYLMEAPYKVIHRDLKSRNVIALDGV-----LKICDFG 153
QY 125 ISRQSFHGAIGVGTGPGYQAPRIPIVYDEKVMFSYGMVLYELLSGQRPALGHQLO 184
DB 154 ASRFNHTTMSLVGTGPGYQAPRIPIVYDEKVMFSYGMVLYELLSGQRPALGHQLO 213
QY 185 IAKKLSKIRPVLCQPEEVOF-----RRLQALMMECWDTPEKRPALSVSQMKDPTFA 239
DB 214 VAWL-----VVEKNERLITPSSCPSPFAELHQCWEADAKKPSFKQIISLESMSND 266
QY 240 TFWYELC 246
DB 267 TSLPDKC 273

RESULT 9
US-09-221-527-5
Sequence 5, Application US/09221527
Patent No. 616832
GENERAL INFORMATION:
APPLICANT: Acton, Susan
TITLE OF INVENTION: NOVEL CSAPE-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
FILE REFERENCE: NMI-050
CURRENT APPLICATION NUMBER: US/09/221,527
CURRENT FILING DATE: 1998-12-28
EARLIER APPLICATION NUMBER: 09/163,115
EARLIER FILING DATE:
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 455
TYPE: PRT
ORGANISM: Homo sapiens

US-09-221-527-5

Query Match 6.4%; Score 243; DB 3; Length 455;

Best Local Similarity 27.9%; Pred. No. 1.5e-14;

Matches 69; Conservative 52; Mismatches 100; Indels 26; Gaps 7;

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QY 10 AMKNFSEFRQASMLHALQHPCTVALIGISIHPLCFAL--ELAPLSLNTVLSBNARDSS 67
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 43 AVKLLKIEKEAEILSVLSHRNIIQFYGVILEPPNYGIVTEVASLSGYDYNR--SE 100
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 68 FPLGMLTQKIAVOIASGLAYLHK--NIIFCDLSNDILVMSLDVKEHINIKLSDYG 124
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 101 EMDMDHIMTW--ATDVAKGMHYLMEAPVKVIRHDLKSRNVIAADGV----LKICDFG 153
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 125 ISROSFEHAGLVEGTPGYQAPRIIVYDEKVMESYGVLYELLSCORPALGHQLO 184
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 154 ASRFNNHTHMSLVGTFPMMAPEVIGSLPVSECTDTYSYGVLMEMLTREVPEKGLGLO 213
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 185 IAKLSKGIKIRPVLGQPEEVQF-----RRLQALMMECDTKREKPLALSVSQKDPPTFA 239
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 214 VAWL-----VVEKNERLTIIPSSCFRSPFAELLHQCEWADAKKPSFKQIISLESMSND 266
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 240 TFWYELC 246
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 267 TSLPDKC 273
```

RESULT 10

US-09-221-236-5

Sequence 5, Application US/09221236

Patent No. 6146841

GENERAL INFORMATION:

APPLICANT: Acton, Susan

TITLE OF INVENTION: NOVEL CSAFK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR

FILE REFERENCE: NMT-050

CURRENT APPLICATION NUMBER: US/09/221,236

CURRENT FILING DATE: 1998-12-28

EARLIER APPLICATION NUMBER: 09/163,115

EARLIER FILING DATE: 1998-09-29

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5

LENGTH: 455

TYPE: PRT

ORGANISM: Homo sapiens

US-09-221-236-5

Query Match

Best Local Similarity 27.9%; Score 243; DB 3; Length 455;

Matches 69; Conservative 52; Mismatches 100; Indels 26; Gaps 7;

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QY 10 AMKNFSEFRQASMLHALQHPCTVALIGISIHPLCFAL--ELAPLSLNTVLSBNARDSS 67
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 43 AVKLLKIEKEAEILSVLSHRNIIQFYGVILEPPNYGIVTEVASLSGYDYNR--SE 100
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 68 FPLGMLTQKIAVOIASGLAYLHK--NIIFCDLSNDILVMSLDVKEHINIKLSDYG 124
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 101 EMDMDHIMTW--ATDVAKGMHYLMEAPVKVIRHDLKSRNVIAADGV----LKICDFG 153
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 125 ISROSFEHAGLVEGTPGYQAPRIIVYDEKVMESYGVLYELLSCORPALGHQLO 184
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 154 ASRFNNHTHMSLVGTFPMMAPEVIGSLPVSECTDTYSYGVLMEMLTREVPEKGLGLO 213
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 185 IAKLSKGIKIRPVLGQPEEVQF-----RRLQALMMECDTKREKPLALSVSQKDPPTFA 239
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 214 VAWL-----VVEKNERLTIIPSSCFRSPFAELLHQCEWADAKKPSFKQIISLESMSND 266
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 240 TFWYELC 246
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 267 TSLPDKC 273
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RESULT 11

US-09-221-416-5

Sequence 5, Application US/09221416

Patent No. 6153417

GENERAL INFORMATION:

APPLICANT: Acton, Susan

TITLE OF INVENTION: NOVEL CSAFK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR

FILE REFERENCE: NMT-050

CURRENT APPLICATION NUMBER: US/09/221,416

CURRENT FILING DATE: 1998-12-28

EARLIER APPLICATION NUMBER: 09/163,115

EARLIER FILING DATE: 1998-09-29

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5

LENGTH: 455

TYPE: PRT

ORGANISM: Homo sapiens

US-09-221-416-5

Query Match

Best Local Similarity 27.9%; Score 243; DB 3; Length 455;

Matches 69; Conservative 52; Mismatches 100; Indels 26; Gaps 7;

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QY 10 AMKNFSEFRQASMLHALQHPCTVALIGISIHPLCFAL--ELAPLSLNTVLSBNARDSS 67
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 43 AVKLLKIEKEAEILSVLSHRNIIQFYGVILEPPNYGIVTEVASLSGYDYNR--SE 100
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 68 FPLGMLTQKIAVOIASGLAYLHK--NIIFCDLSNDILVMSLDVKEHINIKLSDYG 124
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 101 EMDMDHIMTW--ATDVAKGMHYLMEAPVKVIRHDLKSRNVIAADGV----LKICDFG 153
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 125 ISROSFEHAGLVEGTPGYQAPRIIVYDEKVMESYGVLYELLSCORPALGHQLO 184
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 154 ASRFNNHTHMSLVGTFPMMAPEVIGSLPVSECTDTYSYGVLMEMLTREVPEKGLGLO 213
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 185 IAKLSKGIKIRPVLGQPEEVQF-----RRLQALMMECDTKREKPLALSVSQKDPPTFA 239
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 214 VAWL-----VVEKNERLTIIPSSCFRSPFAELLHQCEWADAKKPSFKQIISLESMSND 266
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 240 TFWYELC 246
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 267 TSLPDKC 273
```

RESULT 12

US-09-221-245-5

Sequence 5, Application US/09221245

Patent No. 6180358

GENERAL INFORMATION:

APPLICANT: Acton, Susan

TITLE OF INVENTION: NOVEL CSAFK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR

FILE REFERENCE: NMT-050

CURRENT APPLICATION NUMBER: US/09/221,245

CURRENT FILING DATE: 1998-12-28

EARLIER APPLICATION NUMBER: US 09/163,115

EARLIER FILING DATE: 1998-09-29

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5

LENGTH: 455

TYPE: PRT

ORGANISM: Homo sapiens

US-09-221-245-5

Query Match

Best Local Similarity 27.9%; Score 243; DB 3; Length 455;

Matches 69; Conservative 52; Mismatches 100; Indels 26; Gaps 7;

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   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 43 AVKLLKIEKEAEILSVLSHRNIIQFYGVILEPPNYGIVTEVASLSGYDYNR--SE 100
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 68 FPLGMLTQKIAVOIASGLAYLHK--NIIFCDLSNDILVMSLDVKEHINIKLSDYG 124
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Db      101 EMDMDHIMTW--ATDVAKGMHYLMEAPVKVIHRDLKSRNVVIAADGV-----LKTCDPFG 153
      125 ISROSFEHGALGVEGTGPGYQAPRIYVDEKVMFSYGMVLYELLSGORPALGHHLQ 184
Qy      154 ASRFNHTTHMSLVGTFFPMWAPDEVIGSLPVSETCDTYSYGVVLMEMLTREVPFKGLEGLQ 213
Db      185 IAKKLSKGIKIRPVYLGQPEEVQF-----RRLOALMECNDTPEKRPPLASVVSQMKDPTFA 239
      214 VAWL-----VVEKNERLTIPSSCPSPFAELLHQCEWADAKRPSFKQIISTILESMSND 266
Qy      240 TFMVELC 246
Db      267 TSLPDKC 273
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RESULT 13
US-09-163-115-5
; Sequence 5, Application US/09163115A
; Patent No. 6183962
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: NMI-050
; CURRENT APPLICATION NUMBER: US/09/163,115A
; CURRENT FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-163-115-5
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Best Local Similarity 27.9%; Pred. No. 1.5e-14;
Matches 69; Conservative 52; Mismatches 100; Indels 26; Gaps 7;
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      43 AVKLLKTEKEAEILSVLSHRNIIQFYGVILEPPNYGIVTEYASLSGLDYINSNR--SE 100
Db      68 FIPLGMLTOKIAVQIASGLAYLHK--NIIFCDLKSNDILVMSLDVKEHINIKLSDYG 124
      101 EMDMDHIMTW--ATDVAKGMHYLMEAPVKVIHRDLKSRNVVIAADGV-----LKTCDPFG 153
Qy      125 ISROSFEHGALGVEGTGPGYQAPRIYVDEKVMFSYGMVLYELLSGORPALGHHLQ 184
      154 ASRFNHTTHMSLVGTFFPMWAPDEVIGSLPVSETCDTYSYGVVLMEMLTREVPFKGLEGLQ 213
Db      185 IAKKLSKGIKIRPVYLGQPEEVQF-----RRLOALMECNDTPEKRPPLASVVSQMKDPTFA 239
      214 VAWL-----VVEKNERLTIPSSCPSPFAELLHQCEWADAKRPSFKQIISTILESMSND 266
Qy      240 TFMVELC 246
Db      267 TSLPDKC 273
```

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RESULT 14
US-09-221-528-5
; Sequence 5, Application US/09221528
; Patent No. 6190874
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: NMI-050
; CURRENT APPLICATION NUMBER: US/09/221,528
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-528-5
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Query Match      6.4%; Score 243; DB 3; Length 455;
Best Local Similarity 27.9%; Pred. No. 1.5e-14;
Matches 69; Conservative 52; Mismatches 100; Indels 26; Gaps 7;
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      101 EMDMDHIMTW--ATDVAKGMHYLMEAPVKVIHRDLKSRNVVIAADGV-----LKTCDPFG 153
Qy      125 ISROSFEHGALGVEGTGPGYQAPRIYVDEKVMFSYGMVLYELLSGORPALGHHLQ 184
      154 ASRFNHTTHMSLVGTFFPMWAPDEVIGSLPVSETCDTYSYGVVLMEMLTREVPFKGLEGLQ 213
Db      185 IAKKLSKGIKIRPVYLGQPEEVQF-----RRLOALMECNDTPEKRPPLASVVSQMKDPTFA 239
      214 VAWL-----VVEKNERLTIPSSCPSPFAELLHQCEWADAKRPSFKQIISTILESMSND 266
Qy      240 TFMVELC 246
Db      267 TSLPDKC 273
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RESULT 15
US-09-593-553-5
; Sequence 5, Application US/09593553
; Patent No. 6200770
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: NMI-050
; CURRENT APPLICATION NUMBER: US/09/593,553
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 09/163,115
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-593-553-5
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Query Match      6.4%; Score 243; DB 3; Length 455;
Best Local Similarity 27.9%; Pred. No. 1.5e-14;
Matches 69; Conservative 52; Mismatches 100; Indels 26; Gaps 7;
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Db      68 FIPLGMLTOKIAVQIASGLAYLHK--NIIFCDLKSNDILVMSLDVKEHINIKLSDYG 124
      101 EMDMDHIMTW--ATDVAKGMHYLMEAPVKVIHRDLKSRNVVIAADGV-----LKTCDPFG 153
Qy      125 ISROSFEHGALGVEGTGPGYQAPRIYVDEKVMFSYGMVLYELLSGORPALGHHLQ 184
      154 ASRFNHTTHMSLVGTFFPMWAPDEVIGSLPVSETCDTYSYGVVLMEMLTREVPFKGLEGLQ 213
Db      185 IAKKLSKGIKIRPVYLGQPEEVQF-----RRLOALMECNDTPEKRPPLASVVSQMKDPTFA 239
      214 VAWL-----VVEKNERLTIPSSCPSPFAELLHQCEWADAKRPSFKQIISTILESMSND 266
Qy      240 TFMVELC 246
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Mon Dec 15 08:33:47 2003

us-09-836-392-21.rat

Page 7

Db 267 TSLPDKC 273

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Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2003, 07:15:16 ; Search time 36 Seconds

(without alignments)
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Title: US-09-836-392-21

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Searched: 684280 seqs, 185983659 residues

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Minimum DB seq length: 0

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Post-Processing: Minimum Match 0%

Maximum Match 100%
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Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	3822	100.0	728	US-09-836-392-21	Sequence 21, Appl
2	3574.5	93.5	1987	US-10-132-382-6	Sequence 6, Appl
3	3574.5	93.5	2013	US-10-132-382-2	Sequence 2, Appl
4	3574.5	93.5	2014	US-10-132-382-8	Sequence 8, Appl
5	3574.5	93.5	2040	US-10-132-382-4	Sequence 4, Appl
6	2523	66.0	501	US-10-094-749-1689	Sequence 1689, Ap
7	335.5	8.5	911	US-10-115-482-48	Sequence 48, Appl
8	327.5	8.6	1818	US-10-115-482-50	Sequence 50, Appl
9	327.5	8.6	1818	US-10-335-687A-2	Sequence 2, Appl
10	327.5	8.6	1824	US-10-335-687A-5	Sequence 5, Appl
11	275.5	7.2	1924	US-09-862-027-19	Sequence 19, Appl
12	271	7.1	252	US-09-976-782-41	Sequence 41, Appl
13	271	7.1	254	US-09-976-782-30	Sequence 30, Appl
14	271	7.1	256	US-09-863-776-41	Sequence 41, Appl
15	267.5	7.0	1097	US-10-288-798-12	Sequence 12, Appl

15	263	6.9	1036	US-10-354-358-24	Sequence 24, Appl
17	263	6.9	1036	US-10-014-882-2	Sequence 2, Appl
18	260.5	6.8	847	US-10-143-133-2	Sequence 2, Appl
19	250.5	6.6	765	US-10-128-174-36	Sequence 36, Appl
20	247.5	6.5	765	US-10-128-174-3	Sequence 3, Appl
21	247.5	6.5	765	US-10-128-174-35	Sequence 35, Appl
22	247.5	6.5	765	US-10-128-174-44	Sequence 44, Appl
23	246.5	6.4	765	US-10-128-174-37	Sequence 37, Appl
24	246.5	6.4	765	US-10-128-174-39	Sequence 39, Appl
25	246.5	6.4	765	US-10-128-174-42	Sequence 42, Appl
26	246.5	6.4	823	US-10-128-174-43	Sequence 43, Appl
27	244.5	6.4	823	US-10-376-564-63	Sequence 63, Appl
28	244	6.4	257	US-09-863-776-42	Sequence 42, Appl
29	243.5	6.4	505	US-09-977-269-6	Sequence 6, Appl
30	243.5	6.4	505	US-09-882-610-20	Sequence 20, Appl
31	243.5	6.4	505	US-09-877-260-6	Sequence 6, Appl
32	243.5	6.4	505	US-09-877-261-6	Sequence 6, Appl
33	243	6.4	455	US-09-757-982-5	Sequence 5, Appl
34	243	6.4	455	US-10-094-749-2477	Sequence 2477, Ap
35	242.5	6.3	850	US-10-128-174-41	Sequence 41, Appl
36	242.5	6.3	850	US-09-804-389-2	Sequence 2, Appl
37	242	6.3	257	US-09-823-187-46	Sequence 46, Appl
38	241.5	6.3	765	US-10-128-174-38	Sequence 38, Appl
39	241.5	6.3	765	US-10-128-174-40	Sequence 40, Appl
40	240.5	6.3	349	US-10-106-698-6345	Sequence 6345, Ap
41	239.5	6.3	765	US-10-128-174-34	Sequence 34, Appl
42	238	6.2	937	US-09-974-298-129	Sequence 129, App
43	237	6.2	425	US-09-828-113-29	Sequence 29, Appl
44	236	6.2	263	US-09-840-704-5	Sequence 5, Appl
45	236	6.2	821	US-10-171-404A-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1
US-09-836-392-21
Sequence 21, Application US/09836392
Patent No. US20020173458A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypept
FILE REFERENCE: PTO2001
CURRENT APPLICATION NUMBER: US/09/836,392
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: PCT/US00/28066
PRIOR FILING DATE: 2000-10-11
PRIOR APPLICATION NUMBER: 60/159,542
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/165,914
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/189,027
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 728
TYPE: PRT
ORGANISM: Homo sapiens
US-09-836-392-21

Query Match
Best Local Similarity 100.0%; Score 3822; DB 10; Length 728;
Matches 728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MLRRATDAMKNSFSEPROEASMLHLPICVALLGISIHPLCPALBLAPISLNTVLS 60
QY 61 ENADSSFILGMLTOKIAIVQIASGLAYLHKNNITFCOLKSDNITWMLDVKEHINTK 120
DB 61 ENADSSFILGMLTOKIAIVQIASGLAYLHKNNITFCOLKSDNITWMLDVKEHINTK 120

QY 121 SDYGISRQSFHEGALGVEGTGPGYQAPERIRIYDEKVMFSYGMVLYELLSSQRPALGH 180
DB 121 SDYGISRQSFHEGALGVEGTGPGYQAPERIRIYDEKVMFSYGMVLYELLSSQRPALGH 180
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DB 181 HOQIARKLSKGRIPVLGQPEEVOFRRLQALMMECWDTKPEKRPPLALSVVSQMDPTFAT 240
QY 241 FMYELCCGKQIAFFSSQGOEYTVFMGKESERNYVNTNTEKGLMEVQRMCCPMKYSQ 300
DB 241 FMYELCCGKQIAFFSSQGOEYTVFMGKESERNYVNTNTEKGLMEVQRMCCPMKYSQ 300
QY 301 LOVQSLMTATEQKIIYITLKGMCPNTPQALDTPAVVTCFLAVPIKKNYSYLAAGL 360
DB 301 LOVQSLMTATEQKIIYITLKGMCPNTPQALDTPAVVTCFLAVPIKKNYSYLAAGL 360
QY 361 ADGLVAVFPVVRGTGTPKDCSYLCSHTANRSKFSIADBDARQNPYVKAMEVNVNNGSEVMY 420
DB 361 ADGLVAVFPVVRGTGTPKDCSYLCSHTANRSKFSIADBDARQNPYVKAMEVNVNNGSEVMY 420
QY 421 SNGPGLVVIDCASLEICRLEPYMAPSMVTSVVCSSBGRGEEVWCLDDKXANSLVMYHST 480
DB 421 SNGPGLVVIDCASLEICRLEPYMAPSMVTSVVCSSBGRGEEVWCLDDKXANSLVMYHST 480
QY 481 TYQLCARYFCGVPSPRLDMFPVRPLDTEPPAASHNTANPKVEBDSIADVSIMYSEELGTQ 540
DB 481 TYQLCARYFCGVPSPRLDMFPVRPLDTEPPAASHNTANPKVEBDSIADVSIMYSEELGTQ 540
QY 541 ILIHQESLTDYCSMSYSSSPPROAARSPPSLPSSPASSSVPSTDCEDSDMLHTPGAA 600
DB 541 ILIHQESLTDYCSMSYSSSPPROAARSPPSLPSSPASSSVPSTDCEDSDMLHTPGAA 600
QY 601 SDRSEHDLTPMDGSETFSQHQAQVXILAVRDLIWPBRGGDVIYVIGLEKDSAOGRVIYAV 660
DB 601 SDRSEHDLTPMDGSETFSQHQAQVXILAVRDLIWPBRGGDVIYVIGLEKDSAOGRVIYAV 660
QY 661 LKARELTPHGVLVDAVAVAADTVCTFENENTEMCLAVRMGMAAREFDIFYGOSYEEELGRL 720
DB 661 LKARELTPHGVLVDAVAVAADTVCTFENENTEMCLAVRMGMAAREFDIFYGOSYEEELGRL 720
QY 721 EACTRKRR 728
DB 721 EACTRKRR 728

RESULT 2
US-10-132-382-6
; Sequence 6, Application US/10132382
; Publication No. US20030045699A1
; GENERAL INFORMATION:
; APPLICANT: WEISS, BERTRAM
; TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROLS
; FILE REFERENCE: SCH-1811
; CURRENT APPLICATION NUMBER: US/10/132,382
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1987
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-382-6

Query Match 93.5%; Score 3574.5; DB 15; Length 1987;
Best Local Similarity 94.5%; Pred. No. 4,4e-296;
Matches 687; Conservative 0; Mismatches 1; Indels 39; Gaps 1;

QY 1300 MCRHLRATDANKNFSERROEASMLHALQHPCTIVALIGISIHPLCFALSLAPLSINTVLS 1359

DB 1300 MCRHLRATDANKNFSERROEASMLHALQHPCTIVALIGISIHPLCFALSLAPLSINTVLS 1359

QY 61 ENARDSFPIPLGHMLTQKIAYQIASGLAYLHKNNIIFCDLKSNDILVMSLDVKEHINIKL 120

DB 61 ENARDSFPIPLGHMLTQKIAYQIASGLAYLHKNNIIFCDLKSNDILVMSLDVKEHINIKL 120

DB 1360 ENARDSFPIPLGHMLTQKIAYQIASGLAYLHKNNIIFCDLKSNDILVMSLDVKEHINIKL 1419
QY 121 SDYGISRQSFHEGALGVEGTGPGYQAPERIRIYDEKVMFSYGMVLYELLSSQRPALGH 180
DB 1420 SDYGISRQSFHEGALGVEGTGPGYQAPERIRIYDEKVMFSYGMVLYELLSSQRPALGH 1479
QY 181 HOQIARKLSKGRIPVLGQPEEVOFRRLQALMMECWDTKPEKRPPLALSVVSQMDPTFAT 240
DB 181 HOQIARKLSKGRIPVLGQPEEVOFRRLQALMMECWDTKPEKRPPLALSVVSQMDPTFAT 240
QY 241 FMYELCCGKQIAFFSSQGOEYTVFMGKESERNYVNTNTEKGLMEVQRMCCPMKYSQ 300
DB 241 FMYELCCGKQIAFFSSQGOEYTVFMGKESERNYVNTNTEKGLMEVQRMCCPMKYSQ 300
QY 301 LOVQSLMTATEQKIIYITLKGMCPNTPQALDTPAVVTCFLAVPIKKNYSYLAAGL 360
DB 301 LOVQSLMTATEQKIIYITLKGMCPNTPQALDTPAVVTCFLAVPIKKNYSYLAAGL 360
QY 361 ADGLVAVFPVVRGTGTPKDCSYLCSHTANRSKFSIADBDARQNPYVKAMEVNVNNGSEVMY 420
DB 361 ADGLVAVFPVVRGTGTPKDCSYLCSHTANRSKFSIADBDARQNPYVKAMEVNVNNGSEVMY 420
QY 421 SNGPGLVVIDCASLEICRLEPYMAPSMVTSVVCSSBGRGEEVWCLDDKXANSLVMYHST 480
DB 421 SNGPGLVVIDCASLEICRLEPYMAPSMVTSVVCSSBGRGEEVWCLDDKXANSLVMYHST 480
QY 481 TYQLCARYFCGVPSPRLDMFPVRPLDTEPPAASHNTANPKVEBDSIADVSIMYSEELGTQ 540
DB 481 TYQLCARYFCGVPSPRLDMFPVRPLDTEPPAASHNTANPKVEBDSIADVSIMYSEELGTQ 540
QY 541 ILIHQESLTDYCSMSYSSSPPROAARSPPSLPSSPASSSVPSTDCEDSDMLHTPGAA 600
DB 541 ILIHQESLTDYCSMSYSSSPPROAARSPPSLPSSPASSSVPSTDCEDSDMLHTPGAA 600
QY 601 SDRSEHDLTPMDGSETFSQHQAQVXILAVRDLIWPBRGGDVIYVIGLEKDSAOGRVIYAV 660
DB 601 SDRSEHDLTPMDGSETFSQHQAQVXILAVRDLIWPBRGGDVIYVIGLEKDSAOGRVIYAV 660
QY 661 LKARELTPHGVLVDAVAVAADTVCTFENENTEMCLAVRMGMAAREFDIFYGOSYEEELGRL 720
DB 661 LKARELTPHGVLVDAVAVAADTVCTFENENTEMCLAVRMGMAAREFDIFYGOSYEEELGRL 720
QY 721 EACTRKRR 727
DB 721 EACTRKRR 727

RESULT 3
US-10-132-382-2
; Sequence 2, Application US/10132382
; Publication No. US20030045699A1
; GENERAL INFORMATION:
; APPLICANT: WEISS, BERTRAM
; TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROLS
; FILE REFERENCE: SCH-1811
; CURRENT APPLICATION NUMBER: US/10/132,382
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2013
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-382-2

Query Match 93.5%; Score 3574.5; DB 15; Length 2013;
Best Local Similarity 94.5%; Pred. No. 4,5e-296;
Matches 687; Conservative 0; Mismatches 1; Indels 39; Gaps 1;

QY 1326 MCRHLRATDANKNFSERROEASMLHALQHPCTIVALIGISIHPLCFALSLAPLSINTVLS 1385

DB 1326 MCRHLRATDANKNFSERROEASMLHALQHPCTIVALIGISIHPLCFALSLAPLSINTVLS 1385

QY 61 ENARDSFIPLGMLTOKIAYOIASGLAYLHKNTIIFCDLKSNDILWMSLDVKEHINIKL 120
 DB 1386 ENARDSFIPLGMLTOKIAYOIASGLAYLHKNTIIFCDLKSNDILWMSLDVKEHINIKL 1445
 QY 121 SDYGISRQSFHEGALGVEGTGQYAPRIIVYDEKDMFSGVMVYELLISGORPALGH 180
 DB 1446 SDYGISRQSFHEGALGVEGTGQYAPRIIVYDEKDMFSGVMVYELLISGORPALGH 1505
 QY 181 HOLOIAKLSKIRPVLGQPEEVOFRLOALMECMTDTEKREPLALSVSOMKDPFPAT 240
 DB 1506 HOLOIAKLSKIRPVLGQPEEVOFRLOALMECMTDTEKREPLALSVSOMKDPFPAT 1565
 QY 241 FMYELCCGKOTAFSSQGOEYTVFMDGKEBSRNYTVNTEKIMEVORMCPCGMKVSQC 300
 DB 1566 FMYELCCGKOTAFSSQGOEYTVFMDGKEBSRNYTVNTEKIMEVORMCPCGMKVSQC 1625
 QY 301 LOVORSLMTATEDOKIYITLKGMCPLNTPOALDTPAVVTCFLAVPIKNSYLVLAGL 360
 DB 1626 LOVORSLMTATEDOKIYITLKGMCPLNTPOALDTPAVVTCFLAVPIKNSYLVLAGL 1646
 QY 361 ADGLVAVFPVVRGTPKDCSYLCSHTANRKSFIADBDARQNPYPVXAMEVYVNSGSEVMY 420
 DB 1647 ADGLVAVFPVVRGTPKDCSYLCSHTANRKSFIADBDARQNPYPVXAMEVYVNSGSEVMY 1706
 QY 421 SNGPGLVITDCASLEICRLEPYMAPSMVTSVVCSSGEGREVMVCLDDKANSIWMYHST 480
 DB 1707 SNGPGLVITDCASLEICRLEPYMAPSMVTSVVCSSGEGREVMVCLDDKANSIWMYHST 1766
 QY 481 TYQLCARFCGVPSPRLDMFPVRPLDTEPPAASHANPKVPEGDSIADVSIMYSEELGTQ 540
 DB 1767 TYQLCARFCGVPSPRLDMFPVRPLDTEPPAASHANPKVPEGDSIADVSIMYSEELGTQ 1826
 QY 541 ILIHQESLTDYCSMSYSSPPROAARSPSLPSSPASSSVFPTDCEBDMHTPGAA 600
 DB 1827 ILIHQESLTDYCSMSYSSPPROAARSPSLPSSPASSSVFPTDCEBDMHTPGAA 1886
 QY 601 SDRSEHDLTPMDGETFSQHLQAVKILAVRDLIWPBRGQDVITGLEKDSAGRGYIAV 660
 DB 1887 SDRSEHDLTPMDGETFSQHLQAVKILAVRDLIWPBRGQDVITGLEKDSAGRGYIAV 1946
 QY 661 LKARELTPHGVLYDAVAVAKDVVCTFENENTEWCLAVRWGAGAREFDIFYQSYEELGRL 720
 DB 1947 LKARELTPHGVLYDAVAVAKDVVCTFENENTEWCLAVRWGAGAREFDIFYQSYEELGRL 2006
 QY 721 EACTRKR 727
 DB 2007 EACTRKR 2013

RESULT 4
 US-10-132-382-8
 ; Sequence 8, Application US/10132382
 ; Publication No. US20030045699A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WEISS, BERTRAM
 ; TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROLS
 ; FILE REFERENCE: SCH-1811
 ; CURRENT APPLICATION NUMBER: US/10/132.382
 ; CURRENT FILING DATE: 2002-04-26
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 2014
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-132-382-8

Query Match 93.5%; Score 3574.5; DB 15; Length 2014;
 Best Local Similarity 94.5%; Pred. No. 4.5e-296;
 Matches 687; Conservative 0; Mismatches 1; Indels 39; Gaps 1;
 QY 1 MUEHLRATDAMKNFSEFROEASMLHALQHPCTIVALLIGSIHPLCFALTEPLASLNTVLVS 60

DB 1327 MUEHLRATDAMKNFSEFROEASMLHALQHPCTIVALLIGSIHPLCFALTEPLASLNTVLVS 1386
 QY 61 ENARDSFIPLGMLTOKIAYOIASGLAYLHKNTIIFCDLKSNDILWMSLDVKEHINIKL 120
 DB 1387 ENARDSFIPLGMLTOKIAYOIASGLAYLHKNTIIFCDLKSNDILWMSLDVKEHINIKL 1446
 QY 121 SDYGISRQSFHEGALGVEGTGQYAPRIIVYDEKDMFSGVMVYELLISGORPALGH 180
 DB 1447 SDYGISRQSFHEGALGVEGTGQYAPRIIVYDEKDMFSGVMVYELLISGORPALGH 1506
 QY 181 HOLOIAKLSKIRPVLGQPEEVOFRLOALMECMTDTEKREPLALSVSOMKDPFPAT 240
 DB 1507 HOLOIAKLSKIRPVLGQPEEVOFRLOALMECMTDTEKREPLALSVSOMKDPFPAT 1566
 QY 241 FMYELCCGKOTAFSSQGOEYTVFMDGKEBSRNYTVNTEKIMEVORMCPCGMKVSQC 300
 DB 1567 FMYELCCGKOTAFSSQGOEYTVFMDGKEBSRNYTVNTEKIMEVORMCPCGMKVSQC 1626
 QY 301 LOVORSLMTATEDOKIYITLKGMCPLNTPOALDTPAVVTCFLAVPIKNSYLVLAGL 360
 DB 1627 LOVORSLMTATEDOKIYITLKGMCPLNTPOALDTPAVVTCFLAVPIKNSYLVLAGL 1647
 QY 361 ADGLVAVFPVVRGTPKDCSYLCSHTANRKSFIADBDARQNPYPVXAMEVYVNSGSEVMY 420
 DB 1648 ADGLVAVFPVVRGTPKDCSYLCSHTANRKSFIADBDARQNPYPVXAMEVYVNSGSEVMY 1707
 QY 421 SNGPGLVITDCASLEICRLEPYMAPSMVTSVVCSSGEGREVMVCLDDKANSIWMYHST 480
 DB 1708 SNGPGLVITDCASLEICRLEPYMAPSMVTSVVCSSGEGREVMVCLDDKANSIWMYHST 1767
 QY 481 TYQLCARFCGVPSPRLDMFPVRPLDTEPPAASHANPKVPEGDSIADVSIMYSEELGTQ 540
 DB 1768 TYQLCARFCGVPSPRLDMFPVRPLDTEPPAASHANPKVPEGDSIADVSIMYSEELGTQ 1827
 QY 541 ILIHQESLTDYCSMSYSSPPROAARSPSLPSSPASSSVFPTDCEBDMHTPGAA 600
 DB 1828 ILIHQESLTDYCSMSYSSPPROAARSPSLPSSPASSSVFPTDCEBDMHTPGAA 1887
 QY 601 SDRSEHDLTPMDGETFSQHLQAVKILAVRDLIWPBRGQDVITGLEKDSAGRGYIAV 660
 DB 1888 SDRSEHDLTPMDGETFSQHLQAVKILAVRDLIWPBRGQDVITGLEKDSAGRGYIAV 1947
 QY 661 LKARELTPHGVLYDAVAVAKDVVCTFENENTEWCLAVRWGAGAREFDIFYQSYEELGRL 720
 DB 1948 LKARELTPHGVLYDAVAVAKDVVCTFENENTEWCLAVRWGAGAREFDIFYQSYEELGRL 2007
 QY 721 EACTRKR 727
 DB 2008 EACTRKR 2014

RESULT 5
 US-10-132-382-4
 ; Sequence 4, Application US/10132382
 ; Publication No. US20030045699A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WEISS, BERTRAM
 ; TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROLS
 ; FILE REFERENCE: SCH-1811
 ; CURRENT APPLICATION NUMBER: US/10/132.382
 ; CURRENT FILING DATE: 2002-04-26
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 2040
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-132-382-4

Query Match 93.5%; Score 3574.5; DB 15; Length 2040;
 Best Local Similarity 94.5%; Pred. No. 4.6e-296;
 Matches 687; Conservative 0; Mismatches 1; Indels 39; Gaps 1;

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QY      1 MNRHLPATDAMKNSFSEPROEASMLHLOHPCIVALIGISIHPLCEPLAELASLNTVLS 60
Db      1353 MNRHLPATDAMKNSFSEPROEASMLHLOHPCIVALIGISIHPLCEPLAELASLNTVLS 1412
QY      61 ENARDSFTPLGMLTOKTAYOIASGLATLHKNTIIFCDISDNILVMSLWKEHINIKL 120
Db      1413 ENARDSFTPLGMLTOKTAYOIASGLATLHKNTIIFCDISDNILVMSLWKEHINIKL 1472
QY      121 SDYGISROSFEHAGLVEGTGVOAPEIRPIVYDEKVMESYGVNLYELLSGORPALGH 180
Db      1473 SDYGISROSFEHAGLVEGTGVOAPEIRPIVYDEKVMESYGVNLYELLSGORPALGH 1532
QY      181 HOLOIAKLSKIGRPVLGQPEEVOFRLQALMMECDWTKPEKRPPLASVSOQMDPTFAT 240
Db      1533 HOLOIAKLSKIGRPVLGQPEEVOFRLQALMMECDWTKPEKRPPLASVSOQMDPTFAT 1592
QY      241 FMYELCCGKOTAFSSQOGGYTVFWDGKEESRNTVNTKGLMEVQRMCCPGMKVSCQ 300
Db      1593 FMYELCCGKOTAFSSQOGGYTVFWDGKEESRNTVNTKGLMEVQRMCCPGMKVSCQ 1652
QY      301 LOYORSIMWTATEBQKIYITLKMCPINTPOALDTPAVVTCFLAVPIKKNSTVLVAGL 360
Db      1653 LOYORSIMWTATEBQKIYITLKMCPINTPOALDTPAVVTCFLAVPIKKNSTVLVAGL 1673
QY      361 ADGLVAVFPVVRGTPKDCSYLCSHTANKSKFSIADBDARONKPYKAMEVYVNSGSEVWY 420
Db      1674 ADGLVAVFPVVRGTPKDCSYLCSHTANKSKFSIADBDARONKPYKAMEVYVNSGSEVWY 1733
QY      421 SNGPGLLVIDCASLEICRLEPYMASMTVSVYCSSEGESEVWCLDDKANSIWMYHST 480
Db      1734 SNGPGLLVIDCASLEICRLEPYMASMTVSVYCSSEGESEVWCLDDKANSIWMYHST 1793
QY      481 TYOLCARFCGVSPRLDMFPVRPLDTEPPASHTANPVRPGDSIAVSVIYSEBELGTQ 540
Db      1794 TYOLCARFCGVSPRLDMFPVRPLDTEPPASHTANPVRPGDSIAVSVIYSEBELGTQ 1853
QY      541 ILIHOSLTDYCSMSSYSSSPROAARSPSLPSSPASSSVFSTDCEDSDMLHTPPAA 600
Db      1854 ILIHOSLTDYCSMSSYSSSPROAARSPSLPSSPASSSVFSTDCEDSDMLHTPPAA 1913
QY      601 SDRSEHDLTMDDETSGHLOAVKILAVRDLIWRPGDVIYVLEKDSORAGRYAV 660
Db      1914 SDRSEHDLTMDDETSGHLOAVKILAVRDLIWRPGDVIYVLEKDSORAGRYAV 1973
QY      661 LKARELTPHGVLDAAVVAADTVCTFENENTEMCLAVRGGALEFDIFQSYEELGRL 720
Db      1974 LKARELTPHGVLDAAVVAADTVCTFENENTEMCLAVRGGALEFDIFQSYEELGRL 2033
QY      721 EACTRKA 727
Db      2034 EACTRKA 2040

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RESULT 6
US-10-094-749-1689
Sequence 1689, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO

```

APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 08435/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 1689
TYPE: PR
ORGANISM: Homo sapiens
US-10-094-749-1689

```

Query Match 66.0% Score 2523; DB 12; Length 501;
Best Local Similarity 100.0%; Freq. No. 5e-207;
Matches 478; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      160 MFSYGMVLYELSGORPALGHCHQIAKLSKIGRPVLGQPEEVOFRLQALMMECDWTK 219
Db      1 MFSYGMVLYELSGORPALGHCHQIAKLSKIGRPVLGQPEEVOFRLQALMMECDWTK 60
QY      220 PEKRPPLASVSOQMDPTFATFMYELCCGKOTAFSSQOGGYTVFWDGKEESRNTVYN 279
Db      61 PEKRPPLASVSOQMDPTFATFMYELCCGKOTAFSSQOGGYTVFWDGKEESRNTVYN 120
QY      280 TEKGLMEVQRMCCPGMKVSCOLOYORSIMWTATEBQKIYITLKMCPINTPOALDTPAV 339
Db      121 TEKGLMEVQRMCCPGMKVSCOLOYORSIMWTATEBQKIYITLKMCPINTPOALDTPAV 180
QY      340 VTCFLAVPIKKNSTVLVAGLADGLVAVFPVVRGTPKDCSYLCSHTANKSKFSIADEDA 399
Db      181 VTCFLAVPIKKNSTVLVAGLADGLVAVFPVVRGTPKDCSYLCSHTANKSKFSIADEDA 240
QY      400 RQNPYPVYKAMEVYVNSGSEVWYNSNGPGLLVIDCASLEICRLEPYMASMTVSVYCSSEGR 459
Db      241 RQNPYPVYKAMEVYVNSGSEVWYNSNGPGLLVIDCASLEICRLEPYMASMTVSVYCSSEGR 300
QY      460 GEEVWVWCLDDKANSIWMYHSTTYOLCARFCGVSPRLDMFPVRPLDTEPPASHTANPK 519
Db      301 GEEVWVWCLDDKANSIWMYHSTTYOLCARFCGVSPRLDMFPVRPLDTEPPASHTANPK 360
QY      520 VREGDSIADVSIYSEBELGTQILIHOSLTDYCSMSSYSSSPROAARSPSLPSSPASS 579
Db      361 VREGDSIADVSIYSEBELGTQILIHOSLTDYCSMSSYSSSPROAARSPSLPSSPASS 420
QY      580 SSVFSTDCEDSDMLHTPGAASDRSEHDLTMDDETSGHLOAVKILAVRDLIWRPR 637
Db      421 SSVFSTDCEDSDMLHTPGAASDRSEHDLTMDDETSGHLOAVKILAVRDLIWRPR 478

```

RESULT 7
US-10-115-482-48
Sequence 48, Application US/10115482
Publication No. US20030212257A1
GENERAL INFORMATION:

APPLICANT: Spvtek, et al.
TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM
TITLE OF INVENTION: AND METHODS
FILE REFERENCE: 21404-322D
CURRENT APPLICATION NUMBER: US/10/115,482
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/281,086
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR FILING DATE: 2001-04-03

```
/ PRIOR APPLICATION NUMBER: 60/281,863
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/281,906
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/282,934
/ PRIOR FILING DATE: 2001-04-10
/ PRIOR APPLICATION NUMBER: 60/283,512
/ PRIOR FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: 60/285,325
/ PRIOR FILING DATE: 2001-04-19
/ PRIOR APPLICATION NUMBER: 60/285,890
/ PRIOR FILING DATE: 2001-04-23
/ PRIOR APPLICATION NUMBER: 60/286,068
/ PRIOR FILING DATE: 2001-04-24
/ PRIOR APPLICATION NUMBER: 60/286,292
/ PRIOR FILING DATE: 2001-04-25
/ PRIOR APPLICATION NUMBER: 60/287,213
/ PRIOR FILING DATE: 2001-04-27
/ PRIOR APPLICATION NUMBER: 60/288,257
/ PRIOR FILING DATE: 2001-05-02
/ PRIOR APPLICATION NUMBER: 60/291,134
/ PRIOR FILING DATE: 2001-05-15
/ PRIOR APPLICATION NUMBER: 60/282,020
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: 60/291,725
/ PRIOR FILING DATE: 2001-05-17
/ PRIOR APPLICATION NUMBER: 60/294,771
/ PRIOR FILING DATE: 2001-05-31
/ PRIOR APPLICATION NUMBER: 60/296,965
/ PRIOR FILING DATE: 2001-06-08
/ PRIOR APPLICATION NUMBER: 60/299,128
/ PRIOR FILING DATE: 2001-06-08
/ NUMBER OF SEQ ID NOS: 149
/ SEQ ID NO 48
/ LENGTH: 915
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-115-482-48
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```
Query Match      8.8%; Score 335.5; DB 12; Length 915;
Best Local Similarity 26.9%; Pred. No. 1.6e-19;
Matches 106; Conservative 76; Mismatches 159; Indels 53; Gaps 14;
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```
QY 10 AMKNFSE-----PFOEASMLHALQHPCTVALIGISIHPLCFALDELAPLSINTVLSENA 63
DB 238 AVKFNKHTSLRLRQELVVLCHLHPISLSLAAGIRPRMLVMEASGSLDRLLQDQK 357
QY 64 RDSFIFLGHMLTOKIAVOASGLAVLHKNNIFCDLKSNNILVMSLDVKEHINIKLSY 123
DB 358 AS-----LRTLQHRILAHVADGLRYLHSAANIYRDLKPHNVLLFTLYPNAALITAKIADY 412
QY 124 GISROSFHEGALGVGTPGYQAPRI-RPRIYDEKVMFSYGMVLYELL-SGORPALG-- 179
DB 413 GIAQYCCRMGKITSGTGFRAPEVARGNVITNQAADVSGFLLYDILTTGRIYEGIK 472
QY 180 ----HHQLOIAKLSKIGIRPVLGQPEEVOFRRLQALMECHMDTKPEKRPALSVVSQMKD 235
DB 473 FPNFDELEIOGKLPDPVKYGCAP---WPMVEKLTKQCKENPQERPTSAQVDFQVTD 528
QY 236 PTFATFMYELCCGKO-----TAFSSQGGQEVTVFMDG---KEESRYVTVNTE 281
DB 529 ILNSA---ELVCTIRRIILPRQVIVECNVAITHNSRNASTNLGSGHTRDQQLSFLDLNTE 585
QY 282 KGLMEV---QRMCPGKAVSCQLOVQSLM--TATEDOKIYITLKGMCPLNTPQOALDT 336
DB 586 GYTSSEVADSRILCAL---VHLPEKESWIVSGTOSGLTLVINTDEGKKRHLTKWTD 642
QY 337 PAVTTCFLAVPIYK--KNSYLVLAGLADGVAVF 368
DB 643 ---VTCLYCNSEFSKSKOKMFLVGTADGKLAIF 673
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RESULT 8

```
US-10-115-482-50
/ Sequence 50, Application US/10115482
/ Publication No. US20030212257A1
/ GENERAL INFORMATION:
/ APPLICANT: Spylek, et al.
/ TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM
/ TITLE OF INVENTION: AND METHODS
/ FILE REFERENCE: 21404-322D
/ CURRENT FILING DATE: 2002-04-05
/ PRIOR APPLICATION NUMBER: US/10/115,482
/ PRIOR FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: 60/281,136
/ PRIOR FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: 60/281,863
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/281,906
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/282,934
/ PRIOR FILING DATE: 2001-04-10
/ PRIOR APPLICATION NUMBER: 60/283,512
/ PRIOR FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: 60/285,325
/ PRIOR FILING DATE: 2001-04-19
/ PRIOR APPLICATION NUMBER: 60/285,890
/ PRIOR FILING DATE: 2001-04-23
/ PRIOR APPLICATION NUMBER: 60/286,068
/ PRIOR FILING DATE: 2001-04-24
/ PRIOR APPLICATION NUMBER: 60/286,292
/ PRIOR FILING DATE: 2001-04-25
/ PRIOR APPLICATION NUMBER: 60/287,213
/ PRIOR FILING DATE: 2001-04-27
/ PRIOR APPLICATION NUMBER: 60/288,257
/ PRIOR FILING DATE: 2001-05-02
/ PRIOR APPLICATION NUMBER: 60/291,134
/ PRIOR FILING DATE: 2001-05-15
/ PRIOR APPLICATION NUMBER: 60/282,020
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: 60/291,725
/ PRIOR FILING DATE: 2001-05-17
/ PRIOR APPLICATION NUMBER: 60/294,771
/ PRIOR FILING DATE: 2001-05-31
/ PRIOR APPLICATION NUMBER: 60/296,965
/ PRIOR FILING DATE: 2001-05-08
/ PRIOR APPLICATION NUMBER: 60/299,128
/ PRIOR FILING DATE: 2001-06-08
/ NUMBER OF SEQ ID NOS: 149
/ SEQ ID NO 50
/ LENGTH: 911
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-115-482-50

Query Match      8.6%; Score 327.5; DB 12; Length 911;
Best Local Similarity 26.1%; Pred. No. 7.9e-19;
Matches 101; Conservative 75; Mismatches 168; Indels 43; Gaps 13;
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QY 10 AMKNFSE-----PFOEASMLHALQHPCTVALIGISIHPLCFALDELAPLSINTVLSENA 63
DB 238 AVKFNKHTSLRLRQELVVLCHLHPISLSLAAGIRPRMLVMEASGSLDRLLQDQK 357
QY 64 RDSFIFLGHMLTOKIAVOASGLAVLHKNNIFCDLKSNNILVMSLDVKEHINIKLSY 123
DB 358 AS-----LRTLQHRILAHVADGLRYLHSAANIYRDLKPHNVLLFTLYPNAALITAKIADY 412
QY 124 GISROSFHEGALGVGTPGYQAPRI-RPRIYDEKVMFSYGMVLYELL-SGORPALG-- 179
DB 413 GIAQYCCRMGKITSGTGFRAPEVARGNVITNQAADVSGFLLYDILTTGRIYEGIK 472
QY 180 ----HHQLOIAKLSKIGIRPVLGQPEEVOFRRLQALMECHMDTKPEKRPALSVVSQMKD 235
DB 473 FPNFDELEIOGKLPDPVKYGCAP---WPMVEKLTKQCKENPQERPTSAQVDFQVTD 528
```



```

QY 236 PTFATFMYELCCGKOT--AFSSQGEYTVFMDG---KESSRNTVNTKGLMEV- 287
DB 529 AELVCLTRILLPKNVIYECVATHHNSRNASIMLGGCHTDROGLSFLDNTBGTSEEV 588
QY 288 --QRMCCPGMKVSCQLOVORSIM--TATEDOKIYITLKMGCPINTPOALDTPAVYTCF 343
DB 589 ADSRLICLAL---VHLPEKESWISVSGTSGTLVINTEDGKKHTEKMTDS---VTCL 642
QY 344 LAVPVIR--KNSYLVLAGLADGLAVAF 368
DB 643 YCNSFSKOSKOKNFFLVGTADGKLAI 669

```

```

RESULT 9
US-10-335-687A-2
; Sequence 2, Application US/10335687A
; Publication No. US2003016622A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel E.
; TITLE OF INVENTION: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 39267, Human Kinase Family Members and
; FILE REFERENCE: MP102-001PIRNM
; CURRENT APPLICATION NUMBER: US/10/335,687A
; PRIOR FILING DATE: 2003-01-02
; PRIOR FILING DATE: 2002-01-02
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1818
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-687A-2

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Query Match
Best Local Similarity 26.1%; Pred. No. 2,2e-18;
Matches 101; Conservative 75; Mismatches 168; Indels 43; Gaps 13;

QY 10 AMKNPSE-----FROEASMLHALQHPICVIALIGISHPICFALDELAPLSLNTVISENA 63
DB 1201 AVKIFNKHTSLRLROELVVLCHLHHPSLISLAAIGIRPRLVWELASKGSLDRLIQDOK 1260
QY 64 RDSFPIPLGHMLTOKIAVOIASGLAYLHKXNIIIPDLKSDNIIWLSLDVKEHINIKLSIDY 123
DB 1261 AS-----LRTLOHRIALAHVADGLRYLHNSAMIIYRDLKPHNVLLFTLYPNAIIAKIADY 1315
QY 124 GISRQSFHAGALGVEGTGPGYQAPET--RPRIVDEKVDMPFSYGMVLYELL--SGORPALG-- 179
DB 1316 GIAQYCCRMGIKTSEGTGPFRAEVARGNVIVNOQADVYSFGLLYDILTTGGRIIVEGLX 1375
QY 180 ---HHOLOIAKXLSGIRPVAGPEEVOFRLOALMMECMTDKREKRPPLASVSGMKD 235
DB 1376 FPNFDELEIQGLPDPVKEYGAP---WPNVEKLKQCKLENQKRPFAQVFDILNS 1491
QY 236 PTFATFMYELCCGKOT--AFSSQGEYTVFMDG---KESSRNTVNTKGLMEV- 287
DB 1432 AELVCLTRILLPKNVIYECVATHHNSRNASIMLGGCHTDROGLSFLDNTBGTSEEV 1491
QY 288 --QRMCCPGMKVSCQLOVORSIM--TATEDOKIYITLKMGCPINTPOALDTPAVYTCF 343
DB 1492 ADSRLICLAL---VHLPEKESWISVSGTSGTLVINTEDGKKHTEKMTDS---VTCL 1545
QY 344 LAVPVIR--KNSYLVLAGLADGLAVAF 368
DB 1546 YCNSFSKOSKOKNFFLVGTADGKLAI 1572

```

```

RESULT 10
US-10-335-687A-5
; Sequence 5, Application US/10335687A
; Publication No. US2003016622A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel E.
; TITLE OF INVENTION: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 39267, Human Kinase Family Members and
; FILE REFERENCE: MP102-001PIRNM
; CURRENT APPLICATION NUMBER: US/10/335,687A
; PRIOR FILING DATE: 2003-01-02
; PRIOR FILING DATE: 2002-01-02
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1824
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-687A-5

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Query Match
Best Local Similarity 26.1%; Pred. No. 2,2e-18;
Matches 101; Conservative 75; Mismatches 168; Indels 43; Gaps 13;

QY 10 AMKNPSE-----FROEASMLHALQHPICVIALIGISHPICFALDELAPLSLNTVISENA 63
DB 1201 AVKIFNKHTSLRLROELVVLCHLHHPSLISLAAIGIRPRLVWELASKGSLDRLIQDOK 1260
QY 64 RDSFPIPLGHMLTOKIAVOIASGLAYLHKXNIIIPDLKSDNIIWLSLDVKEHINIKLSIDY 123
DB 1261 AS-----LRTLOHRIALAHVADGLRYLHNSAMIIYRDLKPHNVLLFTLYPNAIIAKIADY 1315
QY 124 GISRQSFHAGALGVEGTGPGYQAPET--RPRIVDEKVDMPFSYGMVLYELL--SGORPALG-- 179
DB 1316 GIAQYCCRMGIKTSEGTGPFRAEVARGNVIVNOQADVYSFGLLYDILTTGGRIIVEGLX 1375
QY 180 ---HHOLOIAKXLSGIRPVAGPEEVOFRLOALMMECMTDKREKRPPLASVSGMKD 235
DB 1376 FPNFDELEIQGLPDPVKEYGAP---WPNVEKLKQCKLENQKRPFAQVFDILNS 1491
QY 236 PTFATFMYELCCGKOT--AFSSQGEYTVFMDG---KESSRNTVNTKGLMEV- 287
DB 1432 AELVCLTRILLPKNVIYECVATHHNSRNASIMLGGCHTDROGLSFLDNTBGTSEEV 1491
QY 288 --QRMCCPGMKVSCQLOVORSIM--TATEDOKIYITLKMGCPINTPOALDTPAVYTCF 343
DB 1492 ADSRLICLAL---VHLPEKESWISVSGTSGTLVINTEDGKKHTEKMTDS---VTCL 1545
QY 344 LAVPVIR--KNSYLVLAGLADGLAVAF 368
DB 1546 YCNSFSKOSKOKNFFLVGTADGKLAI 1572

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```

RESULT 11
US-09-862-027-19
; Sequence 19, Application US/09862027
; Patent No. US20020142428A1
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; TITLE OF INVENTION: No. US20020142428A1 Kinases and Uses Thereof
; FILE REFERENCE: 35800/234862
; CURRENT APPLICATION NUMBER: US/09/862,027
; PRIOR FILING DATE: 2001-05-21
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-862-027-19

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Query Match
Best Local Similarity 31.3%; Pred. No. 6,3e-15;

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Matches 78; Conservative 42; Mismatches 92; Indels 37; Gaps 8;

QY 3 RHLRATDAMKNFSERFOEASMTLALQHPCTVALIGI--LCPALPLASLNTVL 60
 Db 33 RHPDEDISQITENYVOEAKLPAMKHPHIIALRVCUKENPLCLVMEFAGGPLYNL 92
 QY 61 ENARDSFPLGHMLTQKI---AYQIASGLAYLHKK---NIFCDLKSNDIILWSL--- 110
 Db 93 -----GKRIIPDLVNMVAQIARGMVYLHDEIVPIIHEDLKSNIILQYEN 141
 QY 111 -DYKEHINIKLSDYIGSRQSFEGALGVEGPGYQAPRIPIRYDEKVMFSYGMVLYS 169
 Db 142 GDLSNKI-LKITDPGLARBEWHTRTKMSAAGTYAWMAPEVIRASMSKSDVMSYGVYLWE 200
 QY 170 LLSGQPALGHHQLQA-----KLSKGRPVLGQPEBVGPRRLQALMECNDTKPEKRP 224
 Db 201 LLTGEVFPFGIDGLRVAIVGMNKIALPIPTCPBP-----PAKLMECDWNPDSRSP 253
 QY 225 LALSVSQM 233
 Db 254 SFTNILDQL 262

RESULT 12
 US-09-976-782-41
 ; Sequence 41, Application US/09976782
 ; Publication No. US20030190715A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Groose et al
 ; TITLE OF INVENTION: No. US20030190715A1el Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-157
 ; CURRENT APPLICATION NUMBER: US/09/976,782
 ; PRIOR FILING DATE: 2001-10-12
 ; PRIOR APPLICATION NUMBER: 60/240,113
 ; PRIOR FILING DATE: 2000-10-12
 ; PRIOR APPLICATION NUMBER: 60/240,662
 ; PRIOR FILING DATE: 2000-10-16
 ; PRIOR APPLICATION NUMBER: 60/240,732
 ; PRIOR FILING DATE: 2000-10-16
 ; PRIOR APPLICATION NUMBER: 60/240,625
 ; PRIOR FILING DATE: 2000-10-16
 ; PRIOR APPLICATION NUMBER: 60/240,703
 ; PRIOR FILING DATE: 2000-10-16
 ; PRIOR APPLICATION NUMBER: 60/241,190
 ; PRIOR FILING DATE: 2000-10-16
 ; PRIOR APPLICATION NUMBER: 60/240,637
 ; PRIOR FILING DATE: 2000-10-16
 ; PRIOR APPLICATION NUMBER: 60/240,669
 ; PRIOR FILING DATE: 2000-10-16
 ; PRIOR APPLICATION NUMBER: 60/262,455
 ; PRIOR FILING DATE: 2001-01-18
 ; PRIOR APPLICATION NUMBER: 60/240,648
 ; PRIOR FILING DATE: 2000-10-16
 ; NUMBER OF SEQ ID NOS: 127
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 41
 ; LENGTH: 252
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:Consensus
 ; OTHER INFORMATION: sequence
 US-09-976-782-41

Query Match 7.1%; Score 271; DB 12; Length 252;
 Best Local Similarity 32.4%; Pred. No. 7.9e-15;
 Matches 78; Conservative 42; Mismatches 93; Indels 28; Gaps 7;

QY 2 LRHLRATDAMKNFSERFOEASMTLALQHPCTVALIGI--SIHPLCFALPLASLNTVL 59
 Db 29 IKILKKSLSSEKKRFLREIQILRSLSHPNIVRLGLVFEEDDHLYLWETMEGGDLFDYL 88
 QY 60 SENARDSFPLGHMLTQKIAYQIASGLAYLHKKNIIIFCDLKSNDIILWSLVDYKEHINIK 119

Db 89 RRNG-----LLSKEAKKIALQILRGLLEYLHSGIVHRDLKENTL-----LDENGTVK 138
 QY 120 LSDYGISRQ---SFEGALGVEGPGYQAPRIPIRYDEKVMFSYGMVLYELLGQRP 176
 Db 139 IADFGIARKLSSSEYKLTFTVGTPPEYMAPEVLEGRYSSKVDVMSLGVILYELLGKLP 198
 QY 177 ALGHQLOIACKLSKGRIPVIGQP-----EYQFRLQALMECNDTKPEKRPALSLV 230
 Db 199 PFGIDPLBELPRIKE--RPLRLPLPNCSEE-----LKDILKCKLNKPEKRPYAKETIL 251
 QY 231 S 231
 Db 252 N 252

RESULT 13
 US-09-976-782-30
 ; Sequence 30, Application US/09976782
 ; Publication No. US20030190715A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Groose et al
 ; TITLE OF INVENTION: No. US20030190715A1el Proteins and Nucleic Acids Encoding
 ; FILE REFERENCE: 21402-157
 ; CURRENT APPLICATION NUMBER: US/09/976,782
 ; PRIOR FILING DATE: 2001-10-12
 ; PRIOR APPLICATION NUMBER: 60/240,113
 ; PRIOR FILING DATE: 2000-10-12
 ; PRIOR APPLICATION NUMBER: 60/240,662
 ; PRIOR FILING DATE: 2000-10-16
 ; PRIOR APPLICATION NUMBER: 60/240,732
 ; PRIOR FILING DATE: 2000-10-16
 ; PRIOR APPLICATION NUMBER: 60/240,625
 ; PRIOR FILING DATE: 2000-10-16
 ; PRIOR APPLICATION NUMBER: 60/240,703
 ; PRIOR FILING DATE: 2000-10-16
 ; PRIOR APPLICATION NUMBER: 60/241,190
 ; PRIOR FILING DATE: 2000-10-16
 ; PRIOR APPLICATION NUMBER: 60/240,637
 ; PRIOR FILING DATE: 2000-10-16
 ; PRIOR APPLICATION NUMBER: 60/240,669
 ; PRIOR FILING DATE: 2000-10-16
 ; PRIOR APPLICATION NUMBER: 60/262,455
 ; PRIOR FILING DATE: 2001-01-18
 ; PRIOR APPLICATION NUMBER: 60/240,648
 ; PRIOR FILING DATE: 2000-10-16
 ; NUMBER OF SEQ ID NOS: 127
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 30
 ; LENGTH: 254
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:Consensus
 ; OTHER INFORMATION: sequence
 US-09-976-782-30

Query Match 7.1%; Score 271; DB 12; Length 254;
 Best Local Similarity 32.4%; Pred. No. 8e-15;
 Matches 78; Conservative 42; Mismatches 93; Indels 28; Gaps 7;

QY 2 LRHLRATDAMKNFSERFOEASMTLALQHPCTVALIGI--SIHPLCFALPLASLNTVL 59
 Db 29 IKILKKSLSSEKKRFLREIQILRSLSHPNIVRLGLVFEEDDHLYLWETMEGGDLFDYL 88
 QY 60 SENARDSFPLGHMLTQKIAYQIASGLAYLHKKNIIIFCDLKSNDIILWSLVDYKEHINIK 119
 Db 89 RRNG-----LLSKEAKKIALQILRGLLEYLHSGIVHRDLKENTL-----LDENGTVK 138
 QY 120 LSDYGISRQ---SFEGALGVEGPGYQAPRIPIRYDEKVMFSYGMVLYELLGQRP 176
 Db 139 IADFGIARKLSSSEYKLTFTVGTPPEYMAPEVLEGRYSSKVDVMSLGVILYELLGKLP 198

QY 177 ALGHQLOIAKLSKGRVVGQP-----EVQFRRIQALMEGMDTKPKRPPLASV 230
DB 199 FPGIDPLELFRKX--RPRRLPLPPNCSE-----LKDLIKKLNKDPEKPTAKEIL 251
QY 231 S 231
DB 252 N 252

RESULT 14

US-09-863-776-41
Sequence 41, Application US/09863776
Publication No. US20030198953A1
GENERAL INFORMATION:
APPLICANT: Spytek, Kimberly A
APPLICANT: Majumder, Kumud
APPLICANT: Tchernev, Velizar T
APPLICANT: Mishra, Vishnu
APPLICANT: Padigaru, Muralidhara
APPLICANT: Spaderu, Steven K
APPLICANT: Shenoy, Suresh G
APPLICANT: Rastelli, Luca
APPLICANT: Li, Li
APPLICANT: Taupier, Raymond J
APPLICANT: Gangolli, Bsha
TITLE OF INVENTION: No. US20030198953A1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-020
CURRENT APPLICATION NUMBER: US/09/863,776
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 09/540,763
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/206,679
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 60/206,688
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 60/206,829
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 60/207,748
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 60/207,798
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 60/208,263
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 60/208,831
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: 60/209,451
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 60/210,060
PRIOR FILING DATE: 2000-06-07
PRIOR APPLICATION NUMBER: 60/219,507
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: 60/221,337
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/221,927
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 60/263,135
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263,698
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/263,694
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 155
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 41
LENGTH: 256
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Protein Kinase

US-09-863-776-41
OTHER INFORMATION: domain Consensus Sequence

Query Match

7.1%, Score 271, DB 12, Length 256;

Best Local Similarity 32.4%, Pred. No. 8.1e-15;
Matches 78; Conservative 42; Mismatches 93; Indels 28; Gaps 7;
QY 2 LHHLRATAMKNFESEFOASMLALOPICVALIGI--SIHPLCPALBAPUSINTVL 59
DB 29 IKLKKRSLSEKKRFLREIQILRSHPNIVLGLGVFEDCHLYLWEMWEGDLPDY 88
QY 60 SENARDSFIPVGHVLTOKIAYQIASGLATYLKKNITFCULKSDNILLWSLDVKEHINIK 119
DB 89 RANG-----LHISEKAKKIALQILRGILEYHSGIVHDLKRENTL-----LDENGTVK 138
QY 120 LSDYGISRQ---SPHEGALGVEGTGPGYQAPFIRRIYVDKVMFSYGWLYELLSGQRP 176
DB 139 IADFLARKLSSSEYKLTITVGPEYMAVEYLEGREYSSKVDWMSIGVILYELLGKDP 198
QY 177 ALGHQLOIAKLSKGRVVGQP-----EVQFRRIQALMEGMDTKPKRPPLASV 230
DB 199 FPGIDPLELFRKX--RPRRLPLPPNCSE-----LKDLIKKLNKDPEKPTAKEIL 251
QY 231 S 231
DB 252 N 252

RESULT 15

US-10-288-798-12
Sequence 12, Application US/10288798
Publication No. US20030207299A1
GENERAL INFORMATION:
APPLICANT: BANDMAN, Olga; NGUYEN, Daniel B;
APPLICANT: WALIA, Nardinder K.; HARALIA, April J.A.;
APPLICANT: YAO, Montique G.; GANDHI, Ameena R.;
APPLICANT: GURURAJAN, Rajagopal; DING, Li;
APPLICANT: PATTERSON, Chandra; YU, Henry;
APPLICANT: BAUGHN, Mariah R.; TRISQUELEY, Catherine M.;
APPLICANT: THORNTON, Michael; ELIOTT, Vicki S.;
APPLICANT: LU, Yan; ISON, Craig H.;
APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;
APPLICANT: AZIMZAI, Yalda; BUREILLO, John D.;
APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.;
APPLICANT: RAMKUMAR, Jayalaxmi; WARREN, Bridget A.;
APPLICANT: KARNNEY, Liam; POLICKY, Jennifer L.;
APPLICANT: THANGAVELOU, Kavitha; BOURFORD, Neil
TITLE OF INVENTION: HUMAN KINASES
FILE REFERENCE: PI-0209 USA
CURRENT APPLICATION NUMBER: US/10/288,798
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: PCT/US01/27219
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/240,542
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/238,389
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/236,499
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: US 60/234,902
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 60/233,654
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US 60/231,357
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: US 60/229,873
PRIOR FILING DATE: 2000-08-31
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PERL Program
SEQ ID NO 12
LENGTH: 1097
TYPE: PRT
ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030207299A1 55052990CD1

US-10-268-798-12

Query Match 7.0%; Score 267.5; DB 12; Length 1097;
Best Local Similarity 20.5%; Pred. No. 1.4e-13;
Matches 178; Conservative 114; Mismatches 310; Indels 267; Gaps 35;

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QY 3 RHURATDAMKNEFEPROEASMLALOHPCIVALLIGISTHP--LCFALPLAPLSSINTYLS 60
DB 174 RHDPEDDISQITLNNVQZAKLPAMLNHPNIALRGVCLKEPNLCIMEFARGGGLNRYLS 233
QY 61 ENARDSFTPLGHMLTOKI---AYQIASGLAYLHK--NIIFCLKSDNILLVMSL--- 110
DB 234 -----GRIIPDILVMAVQIARGMNYLLDEALVPIIHRLDKSSNILLQKYN 282
QY 111 -DYKEHINIKLSYGISROSFEHGAIGVEGTGQYQAPETPRIVYDEKVMFSYGMVLYE 169
DB 283 GDLNRI-LKITDFGLAREMHRITTKASAGIYAMMAPEVIRASMFSGSDVMSYGVLLME 341
QY 170 ILSGORPALGHOLQIA-----KLSKGRPVILGOPEEVOFRRLQALMMECDTRPEKRP 224
DB 342 LITGEVPRFGIDGLAVAYGAMNKLALPISTCEP-----FAKLMEDCMNPDPHSRP 394
QY 225 LAISVVSQM-----KDPFA--TPMYELCCGQTAPESSQGEYTVFWD-- 267
DB 395 SFTNILDOLTTIEESGFEMPKDSFHCLODNWKHEI---QEMFDQLAKEKEKELTWEEZ 450
QY 268 -----GKEE--SRNYTVNTEKIME-----VQWCCPGMKYSQCL-QVQRSLM 308
DB 451 LTPALQCKQCEELRRBOELABERIDLERELNIIHQLOEKPRYKRRKGKFRKRL 510
QY 309 TATEDQKIYI-----YTL-----KMCPLNTPQOALDTPAVVTCFLAVPIKNSY 354
DB 511 KIKDGNRISLSPDFQHKFTVQASPTMDKRSKLINSRSPASPTIIPRLAIQLTPGESS 570
QY 355 LV-----LAQLADGLVAVP----- 369
DB 571 KTWGRSSVVPKEGEHEEKRAKKRGTWGPGLQCKELASGDEGLKSLVDGYQWSSA 630
QY 370 --VVRGTPKD-----SCSYLC-SHTANRSKFSI 394
DB 631 PNLVKG-PRSSPALPGFTSLMEMEDSDSGSGESRLQHSPOSYLCIFPRGEDGDP 689
QY 395 ADEDAQNPYPV-----KAMEVNSG--SEWYSNGPGLLVIDC 431
DB 690 SSDGIHEEPTPVNSATSPQLTPTNLSLKRGAHRRCEVALLGCAVLAATGLGFDLLEA 749
QY 432 ASLEICRLLEP-----YMAFSVTSVCSSEGRGEVWCLDDKANSL 474
DB 750 GKQQLPLEPEPPPAAEKKRREGLFQSSSRPRRSTSPSRKLFKKEEPMLLLGDPASL 809
QY 475 VMHSTTYQLCARVFCGVSPPLRD-----MPVRPLDTEPPAASHANPKVBEQDSI 526
DB 810 TLLSLSSISECN---STRSLRSDSDDEIVVEMVSPVEA-PLSPCTHNP-----L 857
QY 527 ADVSI-MYGEELGTQLIHQESLTDYCNMSYSVSSP-----PRQ--AARSPSLSPSPA 577
DB 858 VNVKVERFKRDNQOSTTPTHVTLTTPSQPSHRRTPSDALKPETLLASRPSNGSLSPS 917
QY 578 -----SSSVPPSTDCEDSDMLHTPGAASDRSEHDLTPMDETFSOHLQAVXILAVRDLI 632
DB 918 PGAGESSSFLFFFPVPGQMLKTPSPSRDCEFPRLDPNVVFP----- 963
QY 633 WYPRRGDIVIIGLEKDEAQRGVIANV 661
DB 964 -TPRRW-----NTQODSTLERPKTLEFL 985
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Search completed: December 14, 2003, 07:25:34
Job time : 38 secs

GenCore version 5.1.6
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CM protein - nucleic search, using frame_plus model

Run on: December 14, 2003, 07:21:06 Search time 123 Seconds

(without alignments)
2612.414 Million cell updates/sec

Title: US-09-836-392-21

Perfect score: 3822
Sequence: 1 MURHARDANKMFSEHFG.....IFYSYELGLRLACTRKRR 728

Scoring table: BLOSUM62

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blisum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MIVLEN=0 -MAXLEN=2000000000
-USER=US09836392@cgn 1.1.103 @runat_12122003_142519_1075 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEDUPEY -NEG_SCORES=0 -WAT -DSPBLOCK=100 -LONGLOG
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-FAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

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2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:
5: /cgn2_6/ptodata/2/ina/PCUS.COMB.seq:
6: /cgn2_6/ptodata/2/ina/backfile1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	856	22.4	526	4	US-09-387-212-10	Sequence 10, Appl
2	856	22.4	526	4	US-09-948-802-10	Sequence 10, Appl
3	257.5	6.7	3389	1	US-08-395-580-1	Sequence 1, Appl
4	247	6.5	2770	4	US-08-426-509A-5	Sequence 5, Appl
5	247	6.5	2770	4	US-08-232-545-5	Sequence 5, Appl
6	247	6.5	2770	5	PCT-US95-05008-5	Sequence 5, Appl
7	243.5	6.4	2827	4	US-08-497-723-1	Sequence 1, Appl
8	243.5	6.4	7607	1	US-08-222-616-19	Sequence 19, Appl
9	243.5	6.4	7607	4	US-08-446-648-19	Sequence 19, Appl
10	243.5	6.4	7607	5	PCT-US95-04228-19	Sequence 19, Appl
11	243	6.4	1365	3	US-09-221-235-6	Sequence 6, Appl
12	243	6.4	1365	3	US-09-221-928-6	Sequence 6, Appl

13	243	6.4	1365	3	US-09-221-527-6	Sequence 6, Appl
14	243	6.4	1365	3	US-09-221-236-6	Sequence 6, Appl
15	243	6.4	1365	3	US-09-221-416-6	Sequence 6, Appl
16	243	6.4	1365	3	US-09-221-245-6	Sequence 6, Appl
17	243	6.4	1365	3	US-09-163-115-6	Sequence 6, Appl
18	243	6.4	1365	3	US-09-221-528-6	Sequence 6, Appl
19	243	6.4	1365	3	US-09-553-553-6	Sequence 6, Appl
20	243	6.4	1365	3	US-09-221-237-6	Sequence 6, Appl
21	243	6.4	1119	4	US-09-399-888-1	Sequence 1, Appl
22	243	6.4	2120	3	US-09-221-235-4	Sequence 4, Appl
23	243	6.4	2120	3	US-09-221-928-4	Sequence 4, Appl
24	243	6.4	2120	3	US-09-221-527-4	Sequence 4, Appl
25	243	6.4	2120	3	US-09-221-236-4	Sequence 4, Appl
26	243	6.4	2120	3	US-09-221-416-4	Sequence 4, Appl
27	243	6.4	2120	3	US-09-221-245-4	Sequence 4, Appl
28	243	6.4	2120	3	US-09-163-115-4	Sequence 4, Appl
29	243	6.4	2120	3	US-09-221-528-4	Sequence 4, Appl
30	243	6.4	2120	3	US-09-593-553-4	Sequence 4, Appl
31	243	6.4	2120	3	US-09-221-237-4	Sequence 4, Appl
32	241	6.3	3425	1	US-08-205-018-1	Sequence 1, Appl
33	238	6.2	2595	2	US-08-469-537A-77	Sequence 77, Appl
34	238	6.2	3358	2	US-08-469-537A-104	Sequence 104, App
35	237.5	6.2	2016	3	US-09-132-118-1	Sequence 1, Appl
36	237.5	6.2	2617	3	US-09-161-443-1	Sequence 1, Appl
37	236	6.2	2890	1	US-07-928-464-1	Sequence 1, Appl
38	236	6.2	2890	5	PCT-US93-07347-1	Sequence 1, Appl
39	236	6.2	3033	1	US-08-003-311B-1	Sequence 1, Appl
40	236	6.2	3033	1	US-08-261-432-1	Sequence 1, Appl
41	234.5	6.1	2137	1	US-08-444-005-16	Sequence 16, Appl
42	230	6.0	2598	4	US-09-417-197-110	Sequence 110, App
43	228.5	6.0	1788	4	US-09-529-279-14	Sequence 14, Appl
44	228.5	6.0	1788	4	US-10-158-895-14	Sequence 14, Appl
45	228.5	6.0	2268	1	US-08-444-005-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-387-212-10
Sequence 10, Application US/09387212A
Patent No. 6309849
GENERAL INFORMATION:
APPLICANT: ROBINSON, KEITH E.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
FILE REFERENCE: NMI-090
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 526
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: All occurrences of n indicate any nucleotide
US-09-387-212-10

Alignment Scores:

Pred. No.: 1.76e-74
Score: 856.00
Percent Similarity: 97.69%
Best Local Similarity: 97.69%
Query Match: 22.40%
Gaps: 0

US-09-836-392-21 (1-728) x US-09-387-212-10 (1-526)

QY 99 AspleuyserrarppanlleleuValTTPSeleuAspYallYegluHstleannlle 118
DB 12 GACCTGAGCTGGACACATCTGGTGGTCCCTTGACGTCAGGACACACATC 71
QY 119 LysleuSerAspYrYglYlleSerAsglnSerPheHsIcgluYalaleuYValgu 138

Db	72	AACGATCTGCATCAGCGGATTTCGAGGCGACTATTCATGAGGCGCGCTGCGTGGAG	1311
Qy	139	GLYThrProGlyTyrGlnAlaProGlnIleArgProArgIleValTyrAspGlnIlyVal	1588
Db	132	GGCAGCTCTGCTACCAAGGCGCCAGAGATCAGAGCCCTCGCATGTATATGAGGAAGTA	1915
Qy	159	AspMetPheSerTyrGlnIleValLeuTyrGlnIleLeuSerGlyGlnArgProAlaLeu	1787
Db	192	GATATGTTCTCCATGTGAATGGAGTGGCTTCCTCGAGTTGCTGCAGGACAGCCCGCACTG	2515
Qy	179	GLYHisIleGlnIleGlnIleAlaIleLysIleAsnSerGlyIleArgProValLeuGly	1987
Db	252	GGCCACACCAAGCTCCAGATTGCCAAGAGAGCTGTCCAAAGGCGATCCGCCCGATTTCTGGGG	3111
Qy	199	GlnProGlnIleValGlnPheArgArgLeuGlnAlaLeuMetMetGluCysTyrAspThr	2185
Db	312	CAGCGGAGGAAGATCGAGCTTCGGGCACATCGAGGCGGCTCTATATGAGATGCTGGGACACT	3711
Qy	219	LysProGlnIlyLysArgProLeuAlaLeuSerValValSerGlnMetLysAspProThr	2385
Db	372	AAGCACAAGAGAGCAACACTGGCGCCCTGTCGGTGGTAGAACCGAGATGAAGAGACCCGACTT	4315
Qy	238	exaIaThrPheMetTyrGlnLeuCysCysGlyIlySerGlnThrAlaPhePheSerSerGln	2585
Db	432	TGCACACTTCATATATATGAACCTGGCTGTGGGAAGACAGACGCTTCCTTCATCATTCCACG	4915
Qy	258	IlyGlnIlyTyrThrValValPheThrPaspGly	268
Db	492	GCCAGAGATACACTGGGGTGTGTTTGGAGTGA	524

RESULT 2

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US-09-948-802-10
Sequence 10, Application US/09948802
Patent No. 6465232
GENERAL INFORMATION:
APPLICANT: ROBISON, KEITH E.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
FILE REFERENCE: NMI-090
CURRENT APPLICATION NUMBER: US/09/948,802
CURRENT FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 09/387,212
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 526
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
OTHER INFORMATION: All occurrences of n indicate any nucleotide
US-09-948-802-10

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Alignment Scores:

Pred. No.:	1 76e-74	length:	356
Score:	856.00	Matches:	16
Percent Similarity:	97.69%	Conservative:	0
Best Local Similarity:	97.69%	Mismatches:	1
Query Match:	22.40%	Indels:	0
DB:	4	Gaps:	3

US-09-836-392-21 (1-728) x US-09-948-802-10 (1-526)

QY 99 AspLeuLysSerAspAsnIleLeuValITPSeLeuAspValLysLH:stleLeuIle 116
Db 12 GACCTGAAGTCGACACATCTTCGTGTGTCCTTCGATCGAAGAGACATCAACATC 71
QY 119 LysLeuSerAspTyrGlyIleSerArgInsPheHisGluGlyAlaLeuGlyValGlu 136
Db 72 AAGCTATCTTACACGGGATTTGAGAGCACTATTCATGACAGAGGCGCCCTTAAGCTGGAG 131
QY 139 GlyThrProGlyTyrGlnAlaProGluIleArgProArgIleValTyrAspGluIleVal 156

Db	132	GGACATCCTGGCTACACAGGCCCCACAGATCAAGGCTGGCATTTATATGATGAGAAAGTA	191
Qy	159	AspMetPheSerTyrGlyMetValLeuTyrGluLeuLeuSerGlyGlnAlaGProAlaLeu	178
Db	192	GAAATATTTCTCTTAAGAAATGGTGTCTTCAACAAGTTGCTGTCAAGACAGCCCTGTGACATG	251
Qy	179	GlyHisHisGluLeuGlnIleAlaLeuLysLeuSerTyrGlyIleArgProValLeuGly	198
Db	252	GGGCACACACCAAGTCCAGATGCCACAGAAAGCTGTCCAAAGGCATCCGCCGGTTCGGGG	311
Qy	199	GlnProGluGluValGlnPheArgArgLeuGlnAlaLeuMetMetGluCysTTPasPTrh	218
Db	312	CACCCGAGAGAGTGTGACGTTCCGGGACCTGCAGCGGCTCATGAGAGAGTCTGGGACACT	371
Qy	219	LysProGluLysArgProLeuAlaLeuSerAlaVal-SerGlnMetLysAspProTrhP	238
Db	372	AAACCCAGAAAGACGACACTGGCCTGTGCGTGGTGAAGCCAAATGAAGACCCGAACTTT	431
Qy	238	eaIathrPheMetTyrGluLeuCysCysGlyLysGlnThrAlaPhePhe-SerSerGlnG	258
Db	432	TGCACCTTCATGATGAACTGTGCTGTGGGAAAGACACAGCCTTCTTCATTCATCCAG	491
Qy	258	LysGlnLysTyrThrVal-ValPheTrpAspGly	268
Db	492	GCCAGAGATPACACTGTGGGTGTGTTGGGATGGA	524

RESULT 3

US-08-395-580-1
; Sequence 1, Application US/08395580
; Patent No. 5676945

GENERAL INFORMATION:

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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 K
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/395,5580
FILING DATE: herewith

PRIOR APPLICATION DATA:

FILING DATE: 01-MAR-1994

NAME: Rebecca L. Ralph (formerly Gaumond)

REFERENCE/DOCKET NUMBER: CH-04888

TELEPHONE: 215-568-3100

INFORMATION FOR SEQ ID NO: 1

LENGTH: 3389 base pairs

STRANDEDNESS: double

MOLECULE TYPE: cDNA

NAME/KEY: CDS

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US-08-395-580-1

Alignment Scores:

Pred. No.:	8,66e-15	Length:	3389
Score:	257.50	Matches:	160
Percent Similarity:	32.14%	Conservative:	83
Best Local Similarity:	21.16%	Mismatches:	263
Query Match:	6.74%	Indels:	250
DB:	1	Gaps:	28

US-09-836-392-21 (1-728) x US-08-395-580-1 (1-3389)

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QY 10 AlMeLysAsnPheserGluPheArgin---GluAlaSerMetLeuHisAlaLeuGln 28
DB 546 GCTGTGAAGAGGTGGAGACCTCCAAAGAACCAATCAAGACATTGCCAAAGCTGAAG 605
QY 29 HisProCysIleValAlaLeuIleGlyIleSerIleHisProLeuCysPheAla----- 46
DB 606 CACCCCAACATCATCTTCAAGGGTGTGCACCCAGGCTCCCTGCTACTGCATCCTC 665
QY 47 LeuGluLeuAlaProLeuSerSerLeuAsnThrValLeuSerGluAsnAlaArgAspSer 66
DB 666 ATGAGATTCTGGCCCAAGGCAAGCTGTATAGAGTACTGGGCTGGCCG----- 716
QY 67 SerPheIleProLeuGlyHisMetLeuThrGlnIleAlaTyrgIleAlaSerGly 86
DB 717 -----CCTGTCAACCCCTCTTACTGTTACTGTGCTCCATGGGATGGCTGTGGC 767
QY 87 LeuAlaTyrgLeuHisValYsAsnIleIlePheCysAspLeuIleSerAspAsnIleLeu 106
DB 768 ATGAACTACTGTAAGCTGCACAAAGATATCCAAAGGATCTCAAGTCCCAACATCTCA 827
QY 107 ValTrpSerLeuAspValIleGlyHisIleAsnIleIleYsLeuSerAspTyrgIleSer 126
DB 828 ATCACTACAGACAGATGTG-----GTGAAGATCTCAAGATTGGACATCTCC 872
QY 127 ArgGln---SerPheHisGluGlyAlaLeuGlyValGlyIleTrpProGlyTyrgAla 145
DB 873 AAGAGCTAGTGAACAAGACCAACAGATGTCCTTTCAGGAGACAGAGCCTGGATGGCC 932
QY 146 ProGluIleArgProArgIleValIleTyrgAspGluYsValAspMetPheSerTyrgIleMet 165
DB 933 CTTGAGGTGATCCGCAATGACCTGTGTCTTGAGAGGTGACATCTGCTCTTGGGGTGG 992
QY 166 ValLeuTyrgIleLeuLeuSerGlyGlnArgPro----- 176
DB 993 GTGCTATGGGAAGCTGCTGCTGTGATGCCCTTACAAAGACGTAGATTCCTGACCAT 1052
QY 177 -----AlaLeuGlyHisHisGluLeuGlnIleAlaIleYsLeuSerGlyIleArg 194
DB 1053 ATCTGGGGTGTGGAAAGCAACAGTCTCATCTG----- 1085
QY 195 ProValLeuGlyGlnProGluGluValAlaInPheArgLeuGlnAlaLeuMetGlu 214
DB 1086 CCGTGGCCCTCCAGTGGCCACAGT-----GGTTCAAGATCCCTGCTTGGCAG 1133
QY 215 CysTrpAspThrIleProGluYsArgPro-----LeuAlaLeuSer 228
DB 1134 TCGTGAATGCAAAACCAAGAAATGCCCATCATTCGACAGATCCTGCTGACATCTGGAC 1193
QY 229 ValIleSerGlnMetIleAspProThrPheAlaThrPheMetTyrgIleLeuYsCysGly 248
DB 1194 ATTGCCCTACGCT-----GATGACTCTCCACA 1220
QY 249 LysGlnThrAlaPhePheSerSerGlnIleGln----- 259
DB 1221 CCCAGAGAACTTACTTTAAGTCCCAAGGAGATGGCCGGAGAGAAGTAAACTGCATTT 1280
QY 260 -----GluTyrgThrValIleAlaPhe-Tr 266
DB 1281 GAAAAGATTAAAGTCAAGAAAGGACCTGTGTGCACCGCTCAGAAAGAGAACTGGGTGATGAGG 1340
QY 266 PAspGlyLysGluGlnIleSerArgAsnTyrgThrValValAsnThrGlnIleYsLeuMetGln 286

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DB 1341 AGAAGAGAGAGACTCAGACAGCCCTGACATCAGGAGCACTATGAAGAACTGGAG 1400
QY 286 uValGlnArgMetCysCysProGlyMetIleValSerCysGlnLeuGlnAlaArgse 306
DB 1401 AGAGCAACAACCTGTATATGGAAGCTTAATAGCCCTCATGT-----TG 1442
QY 306 rLeuThrPheAlaThrGluAspGlnIleTyrgIleTyrgThrLeuYsGlyMetCys-P 326
DB 1443 CAGCTGGAACTCCAG-----AGAGGAGACTGCTC 1472
QY 326 rLeuAsnThrProGlnGlnAla-----LeuAspThrProAlaValIleThrCysPheLeu 345
DB 1473 AGCCAGAGCAAGCTTTAGAGCGAGAGGCGCCAGGCTGTCTGAAGCCACCTTCCCGG 1532
QY 345 lavalProValIleIleYsAsnSerTyrgLeuValLeuAlaGlyLeuAlaAspGlyLeu 365
DB 1533 GGCTCTCCGATGGAAACACAATGA----- 1558
QY 365 AlAlaValPheProValValArgGlyThrProYsAspSerCysSerTyrgLeuCysSerH 385
DB 1559 -----GAACCTTATCAAGAGAGGAATGT----- 1582
QY 385 lThrAlaAsnArgSerTyrgPheSerIleAlaAspGluAspAlaArgGlnAsnPro---- 403
DB 1583 -----GCCACAGAACTGTCAACCCCATACCAAG 1613
QY 404 -----TyrgProValIleAlaMetGluVal-----ValAsnSerGlyS 416
DB 1614 CCAATATACCTCAAGGCGAGTCTTCTCCCTTAACATAGACAGCCCTGAAGTGGGTG 1673
QY 416 erGluValIleTrpTyrgSerAsnGlyProGlyLeuLeuValIleAspCysAlaSerLeuGln 436
DB 1674 GGGCTCTCGTGGTGTCTTAAGGCCCCCTTC----- 1705
QY 436 lCysArgArgLeuGlnProTyrgMetAlaProSerMetValThrSerValValCysSerS 456
DB 1706 --ACCAGAGCCAGATGCCCGTGGCAAGACCG-----TCAC 1739
QY 456 erGluGlyArgGlyGluGluValValIleProCysLeuAspAspYsAlaAsnSerLeuVal 476
DB 1740 CGCAAGCCCAAGCCCAAGGAGGCTGTGG----- 1768
QY 476 etTyrgHisSerThrThrTyrgIleLeuCysAlaArgTyrgPheCysGlyValPro----- 493
DB 1769 -----GCACTGCTCGGCTTGTGAAGCTGTGCCACCCATCAACCT 1811
QY 494 -----SerProLeuArgAspMetPheProValArgProLeuAspTr 507
DB 1812 GAGAGACCAAGAACCCAGAGGGGCTTAGAGGGGAGACCTCAGCCTGGAGAGCTTCCCT 1871
QY 507 hrGluProProAlaAlaSer-HisThrAlaAsnProYsValProGluIleAspSerIle 526
DB 1872 CCGCGCCCTCGGTGGCTTCATCAT----- 1895
QY 527 AlaAspValSerIleMetTyrgSerGluGluLeuGlyThrGlnIleLeuIleHisGlnGlu 546
DB 1896 -----GACCTCCTGCTCCGCAAAATG 1916
QY 547 SerLeuThrAspTyrgCysSerMetSerTyrgSerSerSerProArgGlnAla----- 565
DB 1917 TCTTCATCGTCCCAAGACCTGTCTGTACAGACACTAGGTCCCGGGGCGGGGAGGCCACA 1976
QY 566 -----AlaArgSerProSerSerLeuPro-----SerSerProAlaAspSer 579
DB 1977 GAGGAGGTGGGATCTTGCTCAACACCTCCGAGGAGTACACCCCAACCAAGTGAAG 2036
QY 580 SerSerValProPheSerThrAspCysGluAspSerAspMetLeuHisThrProGlyAla 599
DB 2037 GGCTCAGCCCTGGCTCACCAGCCCAAGT-----TCACCTGGGGGA 2078
QY 600 AlAspAspArgSerGlnHisAspLeuThrProMetAspGlyGluThrPheSerGlnHis 619

```

Db 2079 GCCMAAGGGAAACCACTCTCTCAGTAGGCGCTGTGAAGT----- 2120
 QY 620 LeuGlnAlaValIleuAlaValArgAspLeuIleTyrValProArgArgGlyGly 639
 Db 2120 ----- 2120
 QY 640 AspValIleValIleGlyLeuGlnIuLysAspSerGluAlaGlnArgGlyArgValIleAla 659
 Db 2121 ---GTGGGCTTCTGTGAAGCTGAAGGAGGAGCACTCAAGCCGGGAGAGAGCCGGGCT 2177
 QY 660 ValLeuLysAlaArgGlnLeuThrProHisGlyValLeuValAspAlaAlaValAla 679
 Db 2178 -----GGTCCAGACCTTGAAGCCCATCTGCTGTACAGGGCTGCCGTACCCGA 2231
 QY 680 LysAspThrValValCysThrPheGluGlnGluAsnThrGlu 693
 Db 2232 AGTCAGAAACGTGCATCTCATCGAAGAGAGAGAGAGAGAG 2273

RESULT 4

US-08-426-509A-5
 Sequence 5: Application US/08426509A
 Patent No. 6326469
 GENERAL INFORMATION:
 APPLICANT: Ulrich, Axel
 APPLICANT: Glisheky, Mikhail
 APPLICANT: Sures, Irman G.
 TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
 TITLE OF INVENTION: TYROSINE KINASES
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York,
 STATE: NY
 COUNTRY: USA
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/426,509A
 FILING DATE: 21-APR-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/232,545
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Cornuzzi, Laura A
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7683-0074-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-790-9090
 TELEFAX: 212-869-9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2770 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 US-08-426-509A-5

Alignment Scores:

Pred. No.: 6.6e-14 Length: 2770
 Score: 247.00 Matches: 99
 Percent Similarity: 44.32% Conservative: 65
 Best Local Similarity: 26.76% Mismatches: 129
 Query Match: 6.46% Indels: 78
 DB: 4 Gaps: 15

US-09-836-392-21 (1-728) x US-08-426-509A-5 (1-2770)

QY 15 SerGluPheArgGlnGluAlaSerMetLeuHisAlaLeuGlnHisProCysIleValAla 34
 Db 1179 AATGACTTCTGAGGAGGCGCACATATATAGAACTTAACATCCAAAGCTTATCCAG 1238
 QY 35 LeuIleGlyIleSerIle-----HisProLeuGlnPheAlaLeuGlnLeuAlaProLeu 52
 Db 1239 CTTTATGCTGTTTGCACCTTTAGAAAGATCCATTTATTTATTTACAGATTGACAGACAT 1298
 QY 53 SerSerLeuAsnThrValLeuSerGluAsnAlaArgAspSerPheIleProLeuGly 72
 Db 1299 GGAAGTCTCGCAAGATATCTC---CAAAATGACACCTGATCAAAAATC----- 1343
 QY 73 HisMetLeuThrGlnIle-----AlaTyrGlnIleAlaSerGlyLeuAlaTyrLeu 90
 Db 1344 ---CATCTGACTCAACAGTGAAGATAGATGCGGACAGGTTCTCTGGAAGGCTTATC 1400
 QY 91 HisLysLysAsnIleIlePheCysAspLeuLysSerAspAsnIleLeuValTyrSerLeu 110
 Db 1401 GAGTCTCGGAACATCACTACAGAGATCTGGCTGCCAAGATGTCTTC----- 1448
 QY 111 AspValLysGluHisIleAsnIleLysLeuSerAspTyrGlyIleSerArg----- 127
 Db 1449 ---GTTGTTGAACATATATCTACAAAGTGCAGATTGAGCTTGCAGAGCTTTTAA 1505
 QY 128 -----GlnSerPheHisGluGlyAlaLeuGlyValGluGlyTyr 140
 Db 1506 GTAGATATGAAGACATCTATGATCTTACACAGAAATTAAGTCCGCGGAGGTGAGCT 1565
 QY 141 ProGlyTyrGlnAlaProGluLysArgProArgIleValTyrAspGlyLysValAspMet 160
 Db 1566 -----GGCCCCGAGGCCCATTCGTAGTAAATTAATTCGACATTAAGTCCGATGTA 1613
 QY 161 PheSerTyrGlyMetValLeuTyrGlyLeuLeuSer---GlyGlnArgProAlaLeuGly 179
 Db 1614 TGCTATTTGGAATCTCTCTTTAAGAATCATTTACTTATGCAAAAGCCTTACAGTGC 1673
 QY 180 HisHisGlnLeuGlnIleAlaLysLeuSerLysGlyTyrArgProValLeuGlyGln 199
 Db 1674 ATGACAGGTGCCAGGTATATCCATGTTGCTCAAAACATATGAA-----CTTCCGCA 1727
 QY 200 ProGluGluValAlaGlnPheArgArgLeuGlnAlaLeuMetGluCysTyrAspThrLys 219
 Db 1728 CATCAACACTGTCCA---CAGCAATTTTACACATCTATGAGTCTGGAATGCAGAG 1784
 QY 220 ProGluLysArgProLeuAlaLeuSerValValSerGlnMetLysAspProThrPheAla 239
 Db 1785 CCTAGGAACGA-----CTTACATTTGAG 1808
 QY 240 ThrPheMetTyrGlnLeuCysCysGlyLysGlnThrAlaPhe----- 254
 Db 1809 AACTGCGTTGGAACCTTGAAGACTATTTGAAACAGA-CTTTCATATTCAAGTGCAGAA 1867
 QY 255 -----SerSerGlnGlyGlnGluTyrThrValAlaPheTyrAspGlyLysGln 270
 Db 1868 TAACCTCATTAAGATGAACACTGGAAGAAATATCAATATTAAGTGAACAACAATTC 1927
 QY 271 Glu-----SerArgAsnTyrThrValValAsnThrGluLysGlyLeuMetGluValGln 288
 Db 1928 AATATATCATTCACAAATATACATATGATATAC----- 1960
 QY 289 ArgMetCysCysProGlyMetLysValSerCysGlnLeuGlnValGlnArgSerLeuTyr 308
 Db 1961 -----CAACTGCACATCATGTTTATTCCTGACA 1987
 QY 309 ThrAlaThrGluAspGlnLysIleTyrIleTyrThrLeuLysGly---MetCysProLeu 327
 Db 1988 TATTCAGATGATAGATTAAGTTGCGCATGATATATGAAAGATTAATTTGTGATTTTA 2047
 QY 328 AsnThrProGlnGlnAlaLeuAspThrProAlaValValThrCysPheLeuAlaValPro 347
 Db 2048 TTGACTGGGCAACACTGACAGACAGTCAAGTCAATATATATGCTACTGCTCGGAGAAA 2107

QY 348 ValIleLysAsnSerTyrlleuValIleu 357
Db 2108 TTAAGCACACTAAACCAAGTATTTCCTT 2137

RESULT 5
US-08-232-545-5
Sequence 5, Application US/08232545
Patent No. 6506578
GENERAL INFORMATION:
APPLICANT: Ulrich, Axel
APPLICANT: Gishizsky, Mikhail
APPLICANT: Sures, Itman G.
TITLE OF INVENTION: No. 6506578e1 Megakaryocytic Protein Tyrosine
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2770 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
US-08-232-545-5

Alignment Scores:
Pred. No.: 6.6e-14 Length: 2770
Score: 247.00 Matches: 99
Percent Similarity: 44.32% Conservative: 65
Best Local Similarity: 26.76% Mismatches: 129
Query Match: 6.46% Indels: 78
Gaps: 15

US-09-836-392-21 (1-728) x US-08-232-545-5 (1-2770)

QY 15 SerGluPheArgGlnGluAlaSerMetLeuHleAlaLeuGlnHisProCysIleValAla 34
Db 1179 AATGACTTCCTGAGGAGGACAGATATATAGAAAGCTAAGACATCAAGCTTATCCAG 1238

QY 35 LeuIleGlyIleSerIle-----HisProLeuGlyPheHleAlaLeuGlnLeuAlaProLeu 52
Db 1239 CTTATATGCTGTTTGCACTTTGAGAGATCCATTATTTATTTACAGAGTTGATGAGACT 1298

QY 53 SerSerLeuAsnThrValLeuSerGluAsnAlaArgSpSerSerPheIleProLeuGly 72
Db 1299 GGAAGCTCGCAAGATATATC-----CAAAATGACACTGATCAAAATATC----- 1343

QY 73 HisMetLeuThrGlnIleValIle-----AlaTyrlGlnIleAlaSerGlyLeuAlaTyrlleu 90
Db 1344 ---CATCTGACTCAACAGGTGACATGCGCGACAGAGTTCCTCTGGAATGGCTTATCTG 1400

QY 91 HisIlySerAsnIleIlePheCysAspLeuLysSerAspAsnIleLeuValTrpSerLeu 110
Db 1401 GAGTCTGGAACCTACATTCACAGATCTGGCTGCCAGAAATGCTCTC----- 1448

QY 111 AspValLysGlnHisIleAsnIleLysLeuSerAspTyrlGlyIleSerArg----- 127
Db 1449 ---CTTGTTGACATTAATATCTACAAAGTACAGATTTTGACCTTGCCAGAGTTTAA 1505

QY 128 -----GlnSerPheHisGlnGlyAlaLeuGlyValGlnGlyThr 140
Db 1506 GTAGATATGAAAGACATCTATGATCTAGACACGAAATAAAGCTGCCGTGAAGTGA 1565

QY 141 ProGlyTyrlGlnAlaProGlnIleArgProArgIleValTyrlAspGlnLysValAspMet 160
Db 1566 -----GGCCCGAAGCCATTCCTGATGAAATTAATTCAGCTTAACTGCAATGTA 1613

QY 161 PheSerTyrlGlyMetValLeuTyrlGlyLeuLeuSer--GlyGlnArgProAlaLeuGly 179
Db 1614 TGCTCATTTGGAAATCCTCTTTATGAATCATTAATTATGACCAAAATGCTTACAGTGT 1673

QY 180 HisIleGlnLeuGlnIleAlaLysLysLeuSerTyrlGlyIleArgProAlaLeuGlyGln 199
Db 1674 ATGACAGCTCCCAAGGATATCCAGATGCTGCCAAACTATAGA-----CTTCGGCA 1727

QY 200 ProGlnGlnValGlnPheArgArgLeuGlnAlaLeuMetGluCysTrpAspThrLys 219
Db 1728 CCATCCCACTGCCA---CAGCAATTTTACAACATCATCTTGAGTGGAGTGGAGATGAGAG 1784

QY 220 ProGlnLysArgProLeuAlaLeuSerValSerGlnMetLysAspProThrPheAla 239
Db 1785 CCTAAGGAACGA-----CCTCATTTTGAG 1808

QY 240 ThrPheMetTyrlGluLeuCysCysGlyLysGlnThrAlaPhePhe----- 254
Db 1809 ACACTGGTTGAAACTGGAAGCTATTTTGAACGA-CTTTATATATTCAGATGCCAA 1867

QY 255 -----SerSerGlnGlyGlnIlyTyrlThrValAlaPheTrpAspGlyLysGln 270
Db 1868 TAACTTCATAGATGACACTGAGAGATATCAAAATATTAAGTAGCAAAATATTC 1927

QY 271 Glu-----SerArgAsnTyrlThrValAlaAsnThrGlnLysGlyLeuMetGlnValGln 288
Db 1928 AATATATCCATTCCTCAAAATATCAATGTTATCAAC----- 1960

QY 289 ArgMetCysCysProGlyMetLysValSerCysGlnLeuGlnValGlnArgSerLeuTrp 308
Db 1961 -----CACTGCACATCATCATTTATCTGACA 1987

QY 309 ThrAlaThrGlnAspGlnLysIleTyrlTyrlThrLeuLysGly---MetCysProLeu 327
Db 1988 TATTCAGATATGAGATTAAGTGGCCATGATATTAAGAAAGATTAATTTTGCAATTTTA 2047

QY 328 AsnThrProGlnGlnAlaLeuAspThrProAlaValAlaThrCysPheLeuAlaValPro 347
Db 2048 TTGACTGGCGACACACGACGACGACGACGATCATATATATTTGCTCACTGCGCTGAAA 2107

QY 348 ValIleLysAsnSerTyrlleuValIleu 357
Db 2108 TTAAGCACACTAAACCAAGTATTTCCTT 2137

RESULT 6
PCT-US95-05008-5
Sequence 5, Application PC/TUS9505008
GENERAL INFORMATION:
APPLICANT: Sugen, Inc.
APPLICANT: 515 Galveston Drive
APPLICANT: Redwood City, California 94063-4720
APPLICANT: United States of America
APPLICANT: Wiesenschaften E.V.
APPLICANT: Hofgarten Str. 2
APPLICANT: Munchen 80539
APPLICANT: Germany

```

/ TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/05008
/ FILING DATE: 24-APR-1995
/ CLASSIFICATION:
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: US 08/232,545
/ FILING DATE: 22-APR-1994
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7663-074
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 869-9741
/ TELEFAX: (212) 869-9741
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2770 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA
/ PCT-US95-05008-5

Alignment Scores:
Pred. No.: 6.6e-14 Length: 2770
Score: 247.00 Matches: 99
Percent Similarity: 44.32% Conservative: 65
Best Local Similarity: 26.76% Mismatches: 129
Query Match: 6.46% Indels: 78
DB: 5 Gaps: 15

US-09-836-392-21 (1-728) x PCT-US95-05008-5 (1-2770)
QY 15 SerGIuPhaArgInGlnAlaSerMetLeuHisAlaLeuGlnHisProCySileValAla 34
DB 1179 AATGACTTCCTGAGGAGGACAGATATATGAAGAACTPAAGACATCCAAAGCTATCCAG 1238
QY 35 LeuIleGlyIleSerIle-----HisProLeuCySPheAlaLeuGlnValLeuAlaProLeu 52
DB 1239 CTTTATGCTGTTGACCTTTAGAAAGATCCAAATTATATTATTAACAGAGTTGATGACACAT 1298
QY 53 SerSerLeuAsnThrValLeuSerGIuAsnAlaArgAspSerPheIleProLeuGly 72
DB 1299 GGAAGCTGCAGAAATATCTC---CAAAATGACACTGATCAAAAAC----- 1343
QY 73 HisMetLeuThrGlnIleValIle-----AlaTyrgInIleAlaSerGIuLeuAlaTyLeu 90
DB 1344 ---CATCTGACTCAACAGGTAGACATGGCGGACAGGTGGCTCTTGAAATGGCCTATCTG 1400
QY 91 HisIleValAsnIleIlePheCyAspLeuIleuYSerAspAsnIleLeuValTrpSerLeu 110
DB 1401 GAGTCGCGAAGTACTTACACAGAGATCTGCTGCGCAGAAATGCTC----- 1448
QY 111 AspValIleGlnHisIleAsnIleIleYSerAspTyrgIleIleSerArg----- 127
DB 1449 ---GTTGGTGAACATATATCTTACAAAGTAGACAGATTTTGACTTGCAGAGTTTAAAG 1505

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QY 128 -----GlnSerPheHisGluGlyAlaLeuGlyValGluGlyThr 140
DB 1506 GTAGATATAGAGACATCTATGATCTAGACAGAAATPAAGTCCGGTGAAGTGAAGT 1565
QY 141 ProGluIleValProGluIleArgProArgIleValIleArgGluIleValAspMet 160
DB 1566 -----GGCCCGAAGCCATTCTGTAATPAATTCAGCATTAAGTCCAGTGA 1613
QY 161 PheSerTyrgIleMetValIleuTyrgIleLeuLeuSer---GlyGlnArgProAlaLeuGly 179
DB 1614 TGGTCAATTGGAAATCCTCTTTATGAATATCTATGAGCAAAATGCTTACAGTGT 1673
QY 180 HisIleGlnLeuGlnIleAlaIleValLeuSerIleGlyIleArgProValLeuGln 199
DB 1674 ATGACAGGTGCCGATATCCAGATGTTGCTCAAAACCTATGA-----CTTCGCA 1727
QY 200 ProGluGluValAlaGlnPheArgArgLeuGlnAlaLeuMetGluCyStrPheThrIle 219
DB 1728 CCATCCAACTGTCCA---CAGCAATTTTACAAATCATGTTGAGAGTGGTGAATGCAAG 1784
QY 220 ProGluIleArgProLeuAlaLeuSerValIleSerGlnMetIleAspProThrPheAla 239
DB 1785 CCTAAGGACGA-----CCTACATTTGAG 1808
QY 240 ThrPheMetTyrgIleuLeuCySylIleGlnThrAlaPhePhe----- 254
DB 1809 AACTGCGTTGGAACTTGAAGACTATTTTGAACAGCA-CTCTTCATATTCAGATGCAAA 1867
QY 255 -----SerSerGlnIleGlnIleuTyrgIleThrValValPheThrAspGlyIleGln 270
DB 1868 TAACATCAATAGATGAAGTCTGAGGAAGATATCAATATATAAGTAGCAAAAACAATTC 1927
QY 271 Glu-----SerArgAsnTyrgIleThrValValAsnThrGlnIleuGlyLeuMetGluValGln 288
DB 1928 AAATPAATCCATTCCAAAATACAAATGATATCAAC----- 1960
QY 289 ArgMetCySProGlyMetIleValSerCySylLeuGlnValAlaArgSerLeuTrp 308
DB 1961 -----CAATGACACATCAGTTTATCTGACA 1987
QY 309 ThrAlaThrGluAspGlnIleIleTyrgIleTyrgIleLeuIleGly---MetCySProLeu 327
DB 1988 TATTCAGATGATAGATTAAGATGGCCATGATATATGAATAATATTATTTGCAATTTTA 2047
QY 328 AsnThrProGlnGlnAlaLeuAspThrProAlaValValThrCySPheLeuAlaValPro 347
DB 2048 TTGACTGGCAACACTGCAGACAGTCAAGTCAATATATGCTCACTGCTGGAATA 2107
QY 348 ValIleIleValAsnSerTyrgLeuValLeu 357
DB 2108 TTAAGCACACTAAACCAAGTATATTTCTT 2137

RESULT 7
US-08-492-723-1
/ Sequence 1, Application US/08492723
/ Patent No. 6531296
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Edison T.
/ APPLICANT: Craven, Rolf J.
/ APPLICANT: Cance, William G.
/ TITLE OF INVENTION: NUCLEAR TYROSINE KINASE PAK
/ NUMBER OF SEQUENCES: 13
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Bell, Seltzer, Park & Gibson
/ STREET: PO Box 34009
/ CITY: Charlotte
/ STATE: North Carolina
/ COUNTRY: USA
/ ZIP: 28234
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/492,723
 FILING DATE:
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Sidley, Kenneth D.
 REGISTRATION NUMBER: 31,665
 REFERENCE/DOCKET NUMBER: 5470-121
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-420-2200
 TELEFAX: 919-881-3175
 INFORMATION FOR SEQ. ID NO. 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2827 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 410..1924
 US-08-492-723-1

Alignment Scores:
 Pred. No.: 1,5e-13 Length: 2827
 Score: 243.50 Matches: 99
 Percent Similarity: 45.25% Conservative: 63
 Best Local Similarity: 27.65% Mismatches: 117
 Query Match: 6.37% Indels: 80
 DB: 4 Gaps: 16

US-09-836-392-21 (1-728) x US-08-492-723-1 (1-2827)

QY 15 SerGlnPheArgGlnGlnAlaSerMetLeuHisAlaLeuGlnHisProCysIleValAla 34
 DB 1223 AATGACTTCCTGAGGGAGGACAGACATTAATGAAGACCTAAGACATCCAAAGCTTATCCAG 1282
 QY 35 LeuIleGlyIleSerIle-----HisProLeuGlyPheAlaLeuGlnAlaProLeu 52
 DB 1283 CTTTATGCTGTTGGACCTTAAAGATCCAAATTATTATTATTACAGAGTTGATAGACAT 1342
 QY 53 SerSerLeuAsnThrValLeuSerGlnAsnAlaArgAspSerPheIleProLeuGly 72
 DB 1343 GGAAGCTCTCAAGAAATATCTC---CAAAATGACACTGATCAAAAATC----- 1387
 QY 73 HisMetLeuThrGlnIleIle-----AlaTyrglnIleAlaSerGlyLeuAlaTyrlleu 90
 DB 1388 ---CATCTGACTCAACAGGTAGACATGGCGGACAGGTTGCTCTGGAATGGCCTATCTG 1444
 QY 91 HisLeuLeuAsnIleIlePheCysAspLeuYsserAspAsnIleLeuValTrpSerLeu 110
 DB 1445 GAGTCTCGAAGTCACTTACAGAGATCTGGCTGCCAAGAAATGCTC----- 1492
 QY 111 AspValIleGlnHisIleAsnIleLeuSerAspTyrgIlyIleSerArg----- 127
 DB 1493 ---GTTGGTGAACATAATATCTCAAGAGAGAGATTGGAAGCTTGGCCAGAGTTTAAAG 1549
 QY 128 -----GlnSerPheHisGlnGlyAlaLeuGlyValGlnGlyThr 140
 DB 1550 GTAGATTAAGAAACATCTATATCAATCAACAGCAAAATAAAGCTTACCGGTGAAGTGAAT 1609
 QY 141 ProGlyTyrglnAlaProGlnIleArgProArgIleValTyraAspGlnTyraAspMet 160
 DB 1610 -----GCCGCCGAACCCATTGTTGTAATAATTAATTAATTAATTAATTAATTAATTA 1657
 QY 161 PheSerTyrglyMetValLeuValLeuLeuSer---GlyGlnArgProAlaLeuGly 119
 DB 1658 TGGTCTTTGGAACTCTCTTTATTAATCAATTAATTAATTAATTAATTAATTAATTAATTA 1717
 QY 180 HisHisGlnLeuGlnIleAlaIleValLeuSerIleGlyIleArgProValLeuGlyGln 199

DB 1718 ATGACAGTGGCCAGGTATCCAGATGTGGCTCAAAACATAGCA-----CTTCCGCAA 1771
 QY 200 ProGlnGlnValGlnPheArgArgLeuGlnAlaLeuMetMetGlnCysTrpAspThrIle 219
 DB 1772 CCATCAACCTGCCA---CAGCATTTTACACATCACTATGTTGAGTCTGCAATGACAG 1828
 QY 220 ProGlnTyraProLeuAlaLeuSerValSerGlnMetIleAspProThrPheAla 239
 DB 1828 CCTAAGAACCA-----CCTACATTTGAG 1852
 QY 240 ThrPheMetTyrglnLeuLeuCysCysGlyIleGlnThrAlaPhePhe----- 254
 DB 1853 ACACCTCGGTGAAACTTGAAGACTATTTCAAAACAGC-CTCTTCATATTCAGATGCAA 1911
 QY 255 -----SerSerGlnGlyGlnGlnTyrglnValValPheTrpAspGlyIleGln 270
 DB 1912 TAACCTCATTAAGATGAACACGAGAAATATCAATTAATAAAGTGAACAAATTC 1971
 QY 271 Gln-----SerArgAsnTyrglnValValAsnThrGlnGlyLeuMetGlnVal 287
 DB 1972 AATATATATCATTCATTCCAAAATACAAATGTTATCAAC----- 2007
 QY 288 GlnArgMetCysCysProGlyMetIleValSerCysGlnLeuGlnValGlnArgSerLeu 307
 DB 2008 -----CACTGCAACATCACTTATCTCTG 2031
 QY 308 TrpThrAlaThrGlnAspGlnIleTyrlleTyrlleTyrlleTyrlleTyrlleTyrlle 326
 DB 2032 ACATATTTAAAGTATAGATTAAGTTAAAGTGGCCATGATTATTAAGTAAAGTATTTGTGAT 2091
 QY 327 LeuAsnThrProGlnGlnAlaLeuAspThrProAlaValAlaThrCysPheLeu 344
 DB 2092 TTATGATCTGGCAACTGTC---AGACACGTCAAGTGATATATATTTCTTC 2142

RESULT 8
 US-08-222-616-19/c
 Sequence 19, Application US/08222616
 Patent No. 5635177
 GENERAL INFORMATION:
 APPLICANT: Bennett, Brian D.
 APPLICANT: Goeddel, David
 APPLICANT: Lee, James M.
 APPLICANT: Matthews, William
 APPLICANT: Teal, Siao Ping
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
 TITLE OF INVENTION: ANTIBODIES
 NUMBER OF SEQUENCES: 42
 CORRESPONDENCE ADDRESS:
 ADDRESS: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd.
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/222,616
 FILING DATE: 4-APR-1994
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/00586
 FILING DATE: 22-JAN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/826935
 FILING DATE: 22-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER:

REFERENCE/DOCKET NUMBER: 821P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-1994
 TELEFAX: 415/952-9881
 TELEEX: 910/371-7168
 INFORMATION FOR SEQ. ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7607 bases
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-222-616-19

Alignment Scores:
 Pred. No.: 7,48e-13 Length: 7607
 Score: 243.50 Matches: 99
 Percent Similarity: 45.38% Conservative: 63
 Best Local Similarity: 27.73% Mismatches: 117
 Query Match: 6.37% Indels: 79
 Gaps: 16

US-09-836-392-21 (1-728) x US-08-222-616-19 (1-7607)

QY 15 SerGluPheArgGlnGluAlaSerMetLeuHisAlaLeuGlnHisProCysIleValAla 34
 Db 2562 AATGACTTCCTGAGGAGGACAGATTAATGAAGACCTTAAGCATCCAAAGCTTATCCAG 2503
 QY 35 LeuIleGlyIleSerIle-----HisProLeuCysPheAlaLeuGlnLeuAlaProLeu 52
 Db 2502 CTTTATGCTGTTGACCTTTAGAGATCCAAATTATTATTATTAAGAGATTATGAGCAT 2443
 QY 53 SerSerLeuAsnThrValLeuSerGluAsnAlaArgAspSerPheIleProLeuGly 72
 Db 2442 GGAAGCTCCAGAAATATCTC---CAAAATGACACTGATCAAAATC----- 2398
 QY 73 HisMetLeuThrGlnIleSile-----AlaIleGlnIleAlaSerGlyLeuAlaIleLeu 90
 Db 2397 ---CATCTGACTCAACAGGTACAGTACGCGGACAGGTGCTCGAATGCTTACTG 2341
 QY 91 HisIleValAsnIleIlePheCysAspLeuIleSerAspAsnIleLeuValIleSerLeu 110
 Db 2340 GAGCTCGGAACTCACTTACAGAGATCTGCTGCCAGAAATGCTC----- 2293
 QY 111 AspValIleGlnHisIleAsnIleIleLeuSerAspIleIleSerArg----- 127
 Db 2292 ---GTTGCTGAACATATATCTTACAAAGTACGAGATTGCTGCGAGATTGTTAAG 2236
 QY 128 -----GlnSerPheHisGlnGlyAlaLeuGlyValGlnGlyThr 140
 Db 2235 GTAGATTAATGAACACTTATGATATCTAGACACGAAATTAAGCTGCGGTGAAGTGAAGT 2176
 QY 141 ProGlyIleGlnAlaProGlyIleArgProArgIleValIleAspGlnIleValAspMet 160
 Db 2175 -----GCGCGGAGGACATGCTAGTAAATTAATTAGATTAAGTCCGAGTGA 2128
 QY 161 PheSerIleGlyMetValLeuIleValLeuLeuSer---GlyGlnArgProAlaLeuGly 179
 Db 2127 TGGTCATTTGGAACTCTCTTTATGAACATTAATCTTATGCGAAATGCTTACAGTGT 2068
 QY 180 HisHisGlnLeuGlnIleAlaIleValIleValIleSerIleGlyIleArgProValIleGln 199
 Db 2067 ATGACAGGTGCCAGGTATCCAGATGTTGCTCAAAACTAAG-----CTTCCGCA 2014
 QY 200 ProGlnGluValGlnPheArgArgIleGlnAlaLeuMetGlnCysIlePhePheIle 219
 Db 2013 CCATCCAACTGTCCA---CAGCAATTTTACAAACATCATGTTGAGTGTGGAAGGAG 1957
 QY 220 ProGluValArgProLeuAlaLeuSerValIleSerGlnMetIleAspProThrPheAla 239
 Db 1956 CTTAAGAGAGA-----CTTACATTTGAG 1933
 QY 240 ThrPheMetIleGlnLeuCysGlyIleValIlePhePhe----- 254

Db 1932 ACACTGCGTGAACCTTGAAGACTATTGAAACAGA-CTTTCATATTCAAGTCCAA 1874
 QY 255 -----SerSerGlnGlyGlnGluIleThrValValPheIlePheArgGlyGlyGlu 270
 Db 1873 TAACCTTAATGAATGAACACTGGAGAGAAATATCAAAATTAAGTGAACAAATTC 1814
 QY 271 Gln-----SerArgAsnIleThrValValAlaMetThrGluIleGlyLeuMetGluValGln 288
 Db 1813 AAATATCATTCATCCAAATTAACATGATATCAAC----- 1781
 QY 289 ArgMetCysProGlyIleMetIleValSerCysGlnLeuGlnValGlnArgSerLeuIle 308
 Db 1780 -----CACTGCACATCACTTATCTGAC 1754
 QY 309 ThrAlaThrGluAspGlnIleIleIleIleIleIleIleIleIleIleIleIleIleIle 327
 Db 1753 TATTCAGTGTAGATGAATGAATGATGCGCATGATATGAAAGATTAATTTGTCATTTA 1694
 QY 328 AsnThrProGlnGlnAlaLeuAspThrProAlaValAlaThrCysPheLeu 344
 Db 1693 TTGACTGGGCAACTGCG---AGACACTCAAGGTGATATTAATTCTCTC 1646

RESULT 9

US-08-446-648-19/C
 Sequence 19, Application US/08446648
 Patent No. 631302

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
 APPLICANT: Bennett, Brian D.
 APPLICANT: Goeddel, David
 APPLICANT: Lee, James M.
 APPLICANT: Matthews, William
 APPLICANT: Tsai, Siao Ping
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/446,648

FILING DATE:

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/222616
 FILING DATE: 04-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P0821P3PCT

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-1994
 TELEFAX: 415/952-9881
 TELEEX: 910/371-7168

INFORMATION FOR SEQ. ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7607 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: Single
 TOPOLOGY: linear

US-08-446-648-19

Alignment Scores:

Pred. No.: 7,48e-13 Length: 7607

Score: 243.50
 Percent Similarity: 45.38%
 Best Local Similarity: 27.73%
 Query Match: 6.37%
 DB: 4
 Matches: 99
 Conservative: 63
 Mismatches: 117
 Indels: 79
 Gaps: 16

US-09-836-392-21 (1-728) x US-08-446-648-19 (1-7607)

QY 15 SerGluPheArgGlnGluAlaSerMetLeuHisAlaLeuGlnHisProCysIleValAla 34
 DB 2562 AATGACTTCCTGAGGAGGACACAGATATGAAGACCTTAAGACATCCAAAGCTTATCCAG 2503
 QY 35 LeuIleGlyIleSerIle-----HisProLeuCysPheAlaLeuGlnLeuAlaProLeu 52
 DB 2502 CTTTATGCTGTTGACCTTTAGACATTCATTTATTTATTTATTCAGAGTTGATGAGACAT 2443
 QY 53 SerSerLeuAsnThrValLeuSerGluAsnAlaArgAspSerPheIleProLeuGly 72
 DB 2442 GGAAGCTGCAAGAAATATCTC---CAAAATGACACTGATCAAAATC----- 2398
 QY 73 HisMetLeuThrGlnIleIle-----AlaTyrGlnIleAlaSerGlyLeuAlaTyrLeu 90
 DB 2397 ---CATCTGACTCAACAGGTAGACATGGCGACAGATGCTCTGAAATGGCTTATCTG 2341
 QY 91 HisLysLysAsnIleIlePheCysAspLeuLysSerAspAsnIleLeuValTyrSerLeu 110
 DB 2340 GAGTCTCGAATACATTCACAGAGATCTGGCTCCAGAAATGCTCTC----- 2293
 QY 111 AspValLysGlnHisIleAsnIleLeuLeuSerAspTyrGlyIleSerArg----- 127
 DB 2292 ---GTTGTGGAACATATATATCTACAAAGTACAGCAATTTGACACTTGCAAGATTTTAA 2236
 QY 128 -----GlnSerPheHisGlnGlyAlaLeuGlyValGlnGlyThr 140
 DB 2235 GTAGATATGAAGACATATGATCTAGACACAAATAAGCTCCCGTGAAGTGAAT 2176
 QY 141 ProGlyTyrGlnAlaProGlnIleArgProArgIleValTyrAspGlnLysValAspMet 160
 DB 2175 -----GGGCCCGAAGCATTCGTATATTAATTAATTCAGCATTAAGTCCAGTGA 2128
 QY 161 PheSerTyrGlyMetValLeuTyrGlnLeuLeuSer-----GlyGlnArgProAlaLeuGly 179
 DB 2127 TGGTCAITTTGGAAATCTCTTTATGAATCATTTATGCGCAAAATGCCCTTACAGTGT 2068
 QY 180 HisHisGlnLeuGlnIleAlaLysLeuSerTyrGlyIleArgProValLeuGlnGly 199
 DB 2067 ATGACAGGTGCCCGATATCCAGATGTGGCTCAAAACATATGA-----CTTCCGCA 2014
 QY 200 ProGlnGlnValGlnPheArgArgLeuGlnAlaLeuMetMetGlyCysTyrAspThrLys 219
 DB 2013 CCATCCAACTGTCCA---CAGCAATTTTACAAACATCTGTTGAGAGTGGATGCGAG 1957
 QY 220 ProGlnLysArgProLeuAlaLeuSerValValSerGlnMetLysAspProThrPheAla 239
 DB 1956 CCTAAGGAACGA-----CCTACATTGAG 1933
 QY 240 ThrPheMetTyrGlnLeuCysCysGlyLysGlnThrAlaPhePhe----- 254
 DB 1932 AACTGCGCTTGGAACTTGAAGACTATTTGAAACAGA-CTCTTCATATTAGATGCAAA 1874
 QY 255 -----SerSerGlnGlyGlnGlyTyrThrValAlaPheThrAspGlyLysGln 270
 DB 1873 TAACTTCATAAGAGACACTGGAGAGAAATATCAATATATTAAGTAAAGCAAAACAATTC 1814
 QY 271 Gln-----SerArgAsnTyrThrValAlaAsnThrGlnLysGlyLeuMetGlnValGln 288
 DB 1813 AAATATATCATTCCAAAATACATATGTTATCAAC----- 1781
 QY 289 ArgMetCysCysProGlnMetLysValSerCysGlnLeuGlnValGlnArgSerLeuTyr 308
 DB 1780 -----CAACTGCAACATCAAGTTATCTGACA 1754
 QY 309 ThrAlaThrGlnAspGlnLysIleTyrIleTyrThrLeuLysGly---MetCysProLeu 327

DB 1753 TATTCAGATGATGATTAAGATTTGGCCCATGTATTAAGAAAAGATTAATTTGCAATTTA 1694
 QY 328 AsnThrProGlnGlnAlaLeuAspThrProAlaValValThrCysPheLeu 344
 DB 1693 TTGACTGGGCAACACTGC---AGACAGTCAAGGTATATATTAATTTCTC 1646

RESULT 10

PCT-US95-04228-19/c

Sequence 19, Application PC/TUS9504228

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Bennett, Brian D.

APPLICANT: Goeddel, David

APPLICANT: Lee, James M.

APPLICANT: Matthews, William

APPLICANT: Tsai, Siao Ping

APPLICANT: Wood, William I.

TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESS: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94095

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: pacin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04228

FILING DATE:

CLASSIFICATION:

Prior Application DATA:

APPLICATION NUMBER: 08/222616

FILING DATE: 04-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Wendy M. Lee

REGISTRATION NUMBER: 00,000

REFERENCE/DOCKET NUMBER: 821P3PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1994

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 7607 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

PCT-US95-04228-19

Alignment Scores:

Pred. No.: 7,48e-13

Score: 243.50

Percent Similarity: 45.38%

Best Local Similarity: 27.73%

Query Match: 6.37%

DB: 5

Length: 7607

Matches: 99

Conservative: 63

Mismatches: 117

Indels: 79

Gaps: 16

US-09-836-392-21 (1-728) x PCT-US95-04228-19 (1-7607)

QY 15 SerGluPheArgGlnGluAlaSerMetLeuHisAlaLeuGlnHisProCysIleValAla 34
 DB 2562 AATGACTTCCTGAGGAGGACACAGATATGAAGACCTTAAGACATCCAAAGCTTATCCAG 2503
 QY 35 LeuIleGlyIleSerIle-----HisProLeuCysPheAlaLeuGlnLeuAlaProLeu 52
 DB 2502 CTTTATGCTGTTGACCTTTAGACATTCATTTATTTATTTATTCAGAGTTGATGAGACAT 2443

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QY      53 SerSerLeuAenTh-ValleuSerGluLeuAlaArgAspSerPheIleProLeuGly 72
DB      2442 GGAAGCTGCAAGAAATATCTC---CAAAATGCACCTGGATAAAAATC----- 2398
QY      73 HisMetLeuThGluAspLeu-----AlaTyrglnIleAlaSerGlyLeuAlaTyrlau 90
DB      2397 ---CATCTACTCAACAGGTAGACATGGCGGACAGGTGGCTCTGGAAAGGCGCTTACTG 2341
QY      91 HisLysLysAsnIleIlePheCysAspLeuLysSerAspAsnIleLeuValTrpSerLeu 110
DB      2340 GAGTCGGAACCTACATTCACAGAGATCTGGCTGCCAAGAAATGTCCTC----- 2293
QY      111 AspValLysGluHisIleAsnIleLysLeuSerAspTyrglyIleSerArg----- 127
DB      2292 ---GTGGTGAACATATATCTACAAAGTAGAGATTTGAGACTTGGCCAGGTTTAAAG 2236
QY      128 -----GlnSerPheHisGluAlaLeuGlyValGluGlyThr 140
DB      2235 GTAGATATAGAAAGACATCTATGATCTAGACACGAAATPAAAGTCCCGGTGAAGTGACT 2176
QY      141 ProGlyTyrglnAlaProGluIleArgProArgIleValTyraAspGluLysValAspMet 160
DB      2175 -----GCCGCCAAGCCCATTCGTAGTAAATTAATTCACCATTAAGTCCGATGTA 2128
QY      161 PheSerTyrglyMetValLeuTyrglyLeuLeuSer---GlyGlnArgProAlaLeuGly 179
DB      2127 TGGTCATTTGGAATCCTCTTTATGAAATCATCTACTTATGGCAAAAGCCCTTACAGTGT 2068
QY      180 HisHisGlnLeuGlnIleAlaLysLysLeuSerLysGlyIleArgProValLeuGlyGln 199
DB      2067 ATGACAGGTGCCAGGTATCCAGATGTTGGCTCAAAACTATAGA-----CTTCCCA 2014
QY      200 ProGluGluValGlnPheArgArgLeuGlnAlaLeuMetMetGlyCysTrpAspThrLys 219
DB      2013 CCAATCACTGTCACA---CAGCAATTTTACACACATCATTTGGAGTGTGGAATGCAGAG 1957
QY      220 ProGluLysArgProLeuAlaLeuSerValValSerGlnMetLysAspProThrPheAla 239
DB      1956 CCAAGAGACGA-----CCTACATTTGAG 1933
QY      240 ThrPheMetTyrglyLeuLysCysGlyLysGlnThrAlaPhePhe----- 254
DB      1932 ACACCTGCGTTGGAACCTGGAAGACATATTTTGAACAGA-CTCTTCATATTCAGATGCAAA 1874
QY      255 -----SerSerGlnGlyGlnGlyLysTyrglnValValPheTrpAspGlyLysGlu 270
DB      1873 TAACCTCATTAAGATGACACTGAGAGAGATATCAATAATTAAGTGCAGAAACAAATTC 1814
QY      271 Glu-----SerArgAsnTyrglnValValAsnThrGluLysGlyLeuMetGluValGln 288
DB      1813 AATAATTCATTCACAAATACATGTTATCAAC----- 1781
QY      289 ArgMetCysCysProGlyMetLysValSerCysGlnLeuGlnValGlnArgSerLeuTrp 308
DB      1780 -----CACTGCACATCACTGTTATCTGACA 1754
QY      309 ThrAlaThrGluAspGlnLysIleTyrlleTyrlleLeuLysGly---MetCysProLeu 327
DB      1753 TATTCAGATGATGATGATTAAGTTGGCCATGTATTTGAAAAGATTATTTGTCATTTTA 1694
QY      328 AsnThrProGlnGlnAlaLeuAspThrProAlaValAlaTrpCysPheLeu 344
DB      1693 TTGACTGGGCAACACTGC---AGGACAGTCAGAGTGATATATATTTCTCTC 1646

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/ CURRENT FILING DATE: 1998-12-28
/ EARLIER APPLICATION NUMBER: 09/163,115
/ EARLIER FILING DATE:
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO: 6
/ LENGTH: 1365
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(1365)
US-09-221-235-6

Alignment Scores:
Pred. No.: 5,13e-14 Length: 1365
Score: 243.00 Matches: 71
Percent Similarity: 49.79% Conservative: 50
Best Local Similarity: 29.22% Mismatches: 104
Query Match: 6.36% Indels: 18
DB: 3 Gaps: 8

US-09-836-392-21 (1-728) x US-09-221-235-6 (1-1365)

QY      10 AlaMetLysAsnPheSerGluPheArgGlnGluAlaSerMetLeuHisAlaLeuGlnHis 29
DB      127 GCTGAAAGAGCTCCCTCAAAATAGAGAGGCAAGATATCTGCTGCTCACTGAC 186
QY      30 ProCysIleValAlaLeuIleGlyIleSerIleHisProLeuCysPheAlaLeu----- 47
DB      187 AGAAACATCATCCAGTTTATGAGTATCTTGAACCTCCACACATGACATGTCACA 246
QY      48 GluLeuAlaProLeuSerSerLeuAenTh-ValleuSerGluLeuAlaArgAspSerSer 67
DB      247 GATATGCTTCTCTGGATCATCTATGATTAATCACTAAGCA-----AGTGG 300
QY      68 PheIleProLeuGlyHisMetLeuThrGlnLysIleAlaTyrglnIleAlaSerGlyLeu 87
DB      301 GAGATGATGATGATCATCATTAATGACCTGG-----GCCACTGATGAGCAAGGAAATG 354
QY      88 AlaTyrglnHisLysLys-----AsnIleIlePheCysAspLeuLysSerAspAsn 104
DB      355 CATTAATTAATGATGAGGCTCCTGTAAGGTGATTCACAGAGACCTCANGTCAAGAAAC 414
QY      105 IleLeuValTrpSerLeuAspValLysGluHisIleAsnIleLysLeuSerAspTyrgly 124
DB      415 GTGTATAGCTGCTGATGAGTA-----CTGAAGATCTGTGACTTTGGT 459
QY      125 IleSerArgGlnSerPheHisGluGlyAlaLeuGlyValGluGlyThrProGlyTyrgln 144
DB      460 GCCCTCGCTGCTCCATTAACCATACACACACATGCTCTGTTGGAACTTTCCCATGATG 519
QY      145 AlaProGluIleArgProArgIleValTyraAspGlyLysValAspMetPheSerTyrgly 164
DB      520 GCTCCAGAGATATCCAGAGATGCCCTGCTGTCAGAAACTGTGACACATATCTATGGT 579
QY      165 MetValLeuTyrglyLeuLeuSerGlyGlnArgProAlaLeuGlyHisHisGlnLeuGln 184
DB      580 GTGGTCTCTCGGAGATGCTTAACAGGAGAGTCCCTTTAAAGTTTGAAGGATTAACA 639
QY      185 IleAla---LysLysLeuSerLysGlyIleArgProValLeuGlnGlnProGluGluVal 203
DB      640 GTAGCTTGCTTGAGTGGAGAAAAAGAGAGAG-----TTAACCATTCACACCACTTGC 693
QY      204 GlnPheArgArgLeuGlnAlaLeuMetMetGlyCysTrpAspThrLysProGlyLysArg 223
DB      694 CCC---AGAGATTGTTGCTGAACCTGTTCAATCAGTGTGGAGACTGATGCCAGAAACGG 750
QY      224 ProLeuAlaLeuSerValValSerGlnMetLysAspProThrPheAlaThrPheMetTyrg 243
DB      751 CCATATTTCAAGCAAAATCATTTCAATCTCTGAGTCCATGCAATGACAGACCTTCTCT 810
QY      244 GluLeuCys 246

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RESULT 11
US-09-221-235-6
; Sequence 6, Application US/0921235
; Patent No. 6043040
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: NMT-050
; CURRENT APPLICATION NUMBER: US/09/221,235

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Db 811 GACAGCTGT 819

RESULT 12
US-09-221-928-6
Sequence 6, Application US/09221928
Patent No. 6121030
GENERAL INFORMATION:
APPLICANT: Acton, Susan
TITLE OF INVENTION: NOVEL CSAFK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
FILE REFERENCE: WNI-050
CURRENT APPLICATION NUMBER: US/09/221,928
CURRENT FILING DATE: 1998-12-28
EARLIER APPLICATION NUMBER: 09/163,115
EARLIER FILING DATE:
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 1365
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1365)
US-09-221-928-6

Alignment Scores:
Pred. No.: 5,136-14 Length: 1365
Score: 243.00 Matches: 71
Percent Similarity: 49.79% Conservative: 50
Best Local Similarity: 29.22% Mismatches: 104
Query Match: 6.36% Indels: 18
DB: 3 Gaps: 8

US-09-836-392-21 (1-728) x US-09-221-928-6 (1-1365)

QY 10 AlAmetLyAsnPheserGluPheargIngluAlaserMetLeuHisAlaleuGlnHis 29
Db 127 GCTGTAAAGAGCTCTCCAAATAGAGAGGCGCAAAATACCTGCTCCAGCTCAC 186
QY 30 ProCysIleValAlaleuIleGlyIleSerIleHisProLeuCysPheAlaleu----- 47
Db 187 AGAACAATCATCCAGTTTATAGAGTATTTCTTAACCTCCCAACTGTGCATTGTGCACA 246
QY 48 GluLeuAlaProLeuSerSerLeuAsnThrValLeuSerGluAsnAlaArgAspSerSer 67
Db 247 GAATATGCTTCTCTGGATCCTCATGATTACATTACAGTAACAGAG-----AGTGAG 300
QY 68 PheIleProLeuGlyHisMetLeuThrGlnIleAlaTyrgInleAlaSerGlyLeu 87
Db 301 GAGATGATATGATCATCATTTATGACTCG-----GCCACTGATGAGCCAAAGAGATG 354
QY 88 AlaTyrgLeuHisLeuLys-----AsnIleIlePheCysAspLeuLysSerAspAsn 104
Db 355 CATATTATACATATGAGAGCTCTGTCAAGGTGATTCACAGAGAGCTCAAGTCAAGAAAC 414
QY 105 IleLeuValTrpSerLeuAspValLysGluHisIleAsnIleLysLeuSerAspTyrgIy 124
Db 415 GTTGTATAGCTGCTGATGAGTA-----CTGAAGATCTGTGACTTTGGT 459
QY 125 IleSerArgInserPheHisGluGlyAlaLeuGlyAlaGluTyrgInleAlaSerGlyLeu 144
Db 460 GCCTCTGCTTCATTAACCATACAAACACATGCTTGGTGGAACTTTCCCATGGAG 519
QY 145 AlaProGluIleArgProArgIleValTyrgPgluLysValAspMetPheSerTyrgIy 164
Db 520 GCTCCAGAGATTATCCAGAGCTCTCTGTCAAAAATTGATCAACATCTTCTTGTGT 579
QY 165 MetValLeuTyrgLeuLeuSerGlyLysArgProAlaLeuGlyHisIleGlnLeuGln 184
Db 580 GTGCTTCTCTGGAGATCTTAACAAGAGAGTCCCTTTAAAGCTTTGGAAGGATTACAA 639
QY 185 IleAla---LysLysLeuSerLysGlyIleArgProValLeuGlyGlnProGluGluVal 203

Db 640 GATGCTGGCTTTAGTGAAGAAAAACAGAGAG-----TTAACCATTCCTCAAGCACTGCC 693
QY 204 GlnPheArgLeuGlnAlaLeuMetMetGluCysTrpAspThrLysProGluLysArg 223
Db 694 CCC---AGAAGTTTGTGTAAGCTTTTCAATCAAGTGTGGAACTGATGCCAAGAAACGG 750
QY 224 ProLeuAlaLeuSerValValSerGlnMetLysAspProThrPheAlaThrPheMetTyrg 243
Db 751 CCATCATTCAGCAAAATCATTCATTCCTGGAGTCCATGTCATCAATGACACAGGCTTCTCT 810
QY 244 GluLeuCys 246
Db 811 GACAGCTGT 819

RESULT 13
US-09-221-527-6
Sequence 6, Application US/09221527
Patent No. 6146832
GENERAL INFORMATION:
APPLICANT: Acton, Susan
TITLE OF INVENTION: NOVEL CSAFK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
FILE REFERENCE: WNI-050
CURRENT APPLICATION NUMBER: US/09/221,527
CURRENT FILING DATE: 1998-12-28
EARLIER APPLICATION NUMBER: 09/163,115
EARLIER FILING DATE:
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 1365
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1365)
US-09-221-527-6

Alignment Scores:
Pred. No.: 5,136-14 Length: 1365
Score: 243.00 Matches: 71
Percent Similarity: 49.79% Conservative: 50
Best Local Similarity: 29.22% Mismatches: 104
Query Match: 6.36% Indels: 18
DB: 3 Gaps: 8

US-09-836-392-21 (1-728) x US-09-221-527-6 (1-1365)

QY 10 AlAmetLyAsnPheserGluPheargIngluAlaserMetLeuHisAlaleuGlnHis 29
Db 127 GCTGTAAAGAGCTCTCCAAATAGAGAGGCGCAAAATACCTGCTCCAGCTCAC 186
QY 30 ProCysIleValAlaleuIleGlyIleSerIleHisProLeuCysPheAlaleu----- 47
Db 187 AGAACAATCATCCAGTTTATAGAGTATTTCTTAACCTCCCAACTGTGCATTGTGCACA 246
QY 48 GluLeuAlaProLeuSerSerLeuAsnThrValLeuSerGluAsnAlaArgAspSerSer 67
Db 247 GAATATGCTTCTCTGGATCCTCATGATTACATTACAGTAACAGAG-----AGTGAG 300
QY 68 PheIleProLeuGlyHisMetLeuThrGlnIleAlaTyrgInleAlaSerGlyLeu 87
Db 301 GAGATGATATGATCATCATTTATGACTCG-----GCCACTGATGAGCCAAAGAGATG 354
QY 88 AlaTyrgLeuHisLeuLys-----AsnIleIlePheCysAspLeuLysSerAspAsn 104
Db 355 CATATTATACATATGAGAGCTCTGTCAAGGTGATTCACAGAGAGCTCAAGTCAAGAAAC 414
QY 105 IleLeuValTrpSerLeuAspValLysGluHisIleAsnIleLysLeuSerAspTyrgIy 124
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QY 125 IleSerArgInserPheHisGluGlyAlaLeuGlyAlaGluTyrgInleAlaSerGlyLeu 144

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QY 30 ProCysIleValaIleuLeuIleGlyIleSerIleHisProLeuCySPheAlaLeu----- 47
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QY 48 GluLeuAlaProIleuSerSerLeuAanThrValLeuSerGIuAsnAlaArgAspSerSer 67
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[illegible]

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RESULT 15
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; Sequence 6, Application US/09221416
; Patent No. 6153417
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: NMT-050
; CURRENT APPLICATION NUMBER: US/09/221,416
; CURRENT FILING DATE: 1998-12-28

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: EARLIER FILING DATE: 1998-09-29
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: NUMBER OF SEQ. ID NOS.: 15
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: SOFTWARE: PatentIn Ver. 2.0
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: SEQ. ID NO. 6
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: LENGTH: 1365
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: TYPE: DNA
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: ORGANISM: Homo sapiens
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NAME/KEY: CDS

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US-09-221-416-6
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Pred. No.: 5,13e-14 Length: 1365
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Best Local Similarity: 29.22% Mismatches: 10
Query Match: 6.36% Indels: 18
DB: 3 Gaps: 8

US-09-836-392-21 (1-728) X US-09-221-416-6 (1-1365)
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: December 14, 2003, 07:24:52 ; Search time 538 Seconds

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4497.361 Million cell updates/sec

Title: US-09-836-392-21

Perfect score: 3822

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Searched: 2201672 seqs, 166179599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Published Applications NA.*
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Prod. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	3579.5	93.7	7015	15	US-10-132-382-5	Sequence 5, Appl1
3	3579.5	93.7	7093	15	US-10-132-382-1	Sequence 1, Appl1
4	3579.5	93.7	7229	15	US-10-132-382-7	Sequence 7, Appl1
5	3579.5	93.7	7307	15	US-10-132-382-3	Sequence 3, Appl1
6	3325	84.4	3112	13	US-10-094-749-50	Sequence 50, Appl1
7	856	22.4	526	15	US-10-121-925-10	Sequence 10, Appl1
8	341.5	8.9	3052	13	US-10-115-482-47	Sequence 47, Appl1
9	330.5	8.6	3040	13	US-10-115-482-49	Sequence 49, Appl1
10	330.5	8.6	5457	13	US-10-335-687A-6	Sequence 6, Appl1
11	330.5	8.6	5475	13	US-10-335-687A-3	Sequence 3, Appl1
12	330.5	8.6	5799	13	US-10-335-687A-1	Sequence 1, Appl1
13	330.5	8.6	5817	13	US-10-335-687A-4	Sequence 4, Appl1
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15	307.5	8.0	3454	13	US-10-171-581-312	Sequence 312, App
16	296.5	7.8	3435	13	US-10-210-120-86	Sequence 86, Appl
17	270.5	7.1	1662	10	US-09-338-842A-1014	Sequence 1014, Ap
18	270.5	7.1	3538	13	US-10-288-798-36	Sequence 36, Appl
19	269.5	7.1	3111	14	US-10-014-882-1	Sequence 1, Appl1
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21	268	7.0	1428	10	US-09-338-842A-882	Sequence 882, App
22	266.5	7.0	5549	13	US-10-354-358-23	Sequence 23, Appl
23	260.5	6.8	3558	14	US-10-143-133-1	Sequence 1, Appl1
24	259.5	6.8	1638	10	US-09-338-842A-903	Sequence 903, App
25	257.5	6.7	3761	13	US-09-814-353-20138	Sequence 20138, A
26	256.5	6.7	3365	15	US-10-153-668-323	Sequence 323, App
27	256.5	6.7	3428	15	US-10-153-668-437	Sequence 437, App
28	253.5	6.6	6378	13	US-10-252-157-482	Sequence 482, App
29	251.5	6.6	2696	13	US-10-128-174-8	Sequence 8, Appl1
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31	251.5	6.6	2696	13	US-10-128-174-10	Sequence 10, Appl
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40	247	6.5	2770	10	US-09-977-269-5	Sequence 5, Appl1
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43	243.5	6.4	7607	10	US-09-982-610-19	Sequence 19, Appl
44	243	6.4	1365	9	US-09-757-982-6	Sequence 6, Appl1
45	243	6.4	2120	9	US-09-757-982-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-09-836-392-8
Sequence 8, Application US/09836392
Patent No. US20020173458A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypept:
FILE REFERENCE: PTO20P1
CURRENT APPLICATION NUMBER: US/09/836,392
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: PCT/US00/26066
PRIOR FILING DATE: 2000-10-11
PRIOR APPLICATION NUMBER: 60/159,542
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/165,914
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/189,027
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentm Ver. 2.0
SEQ ID NO 8
LENGTH: 3496
TYPE: DNA

ORGANISM: Homo sapiens
US-09-836-392-8

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Score: 3822.00 Matches: 728
Percent Similarity: 100.00% Conserved: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-836-392-21 (1-728) X US-09-836-392-8 (1-3496)

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DB 82 GCCAGCATGCTGACCCGCTGCAGCACCCCTGCATCGTGGCGCTCATCGGATCGACATC 141
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QY 81 TyrGlnIleAlaSerGlyLeuAlaTyrLeuHisLysLysAsnIleIlePheCysAspLeu 100
DB 262 TACCAATGCGCTCGGGCTGCGCTACCTGCACAGAAACATCATCTCTGTGACCTG 321
QY 101 LysSerAspAsnIleLeuValTyrSerLeuAspValLysGlnHisIleAsnIleLysLeu 120
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QY 121 SerAspTyrGlyIleSerArgLysPheHisGlnGlyAlaLeuGlyValGlnGlyThr 140
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QY 161 PheSerTyrGlyMetValLeuTyrGlnLeuSerGlyGlnArgProAlaLeuGlyHis 180
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QY 181 HisGlnLeuGlnIleAlaLysLysLeuSerLysGlyIleArgProValLeuGlnPro 200
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DB 622 GAGGAAGTGCAGTTCCGGCGACTGCAGGCGCTCATGATGAGTGTCTGGGACACTAAGCCA 681
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DB 682 GAGAAAGCAGACCGCTGCGCTGTGCGGTGAGCCAGATGAAAGAACCCGACTTTGCCACC 741
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QY 261 TyrThrValValPheTyrAspGlyLysGlnGlnLysArgAsnTyrThrValValAsnThr 280
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Db	2062	GACACTGTGTGTGGACCTTTGAAAATGAAAACAGAGTGTGTGCTCGGCGCTGGAG	2121
Qy	701	GLYTRGIVAlAArgIuPheAspIlePheTyrgInSerTyrgInGluLeuGlyArgLeu	720
Db	2122	GGGTGGGGGGCCAGGAGAGTTCGACATTTTTCACAGCTTCAAGAGAGCTGGGCGGCTG	2181
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; Publication No. US20030045699A1			
; GENERAL INFORMATION:			
; APPLICANT: WEISS, BERTRAM			
; TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROLS			
; FILE REFERENCE: SCH-1811			
; CURRENT APPLICATION NUMBER: US/10/132.382			
; NUMBER OF FILING DATE: 2002-04-26			
; NUMBER OF SEQ. ID NOS: 26			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 5			
; LENGTH: 7015			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
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Percent Similarity: 94.51%			
Best Local Similarity: 94.51%			
Query Match: 93.66%			
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Qy	21	AlaserMetLeuHisAlaLeuGlnHisProCysIleValAlaLeuIleGlyIleSerIle	40
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Qy	61	GluAsnAlaArgAspSerSerPheIleProLeuGlyHisMetLeuThrGlnLysIleAla	80
Db	4304	GAGAAAGCCAGATTCCTTCCTTATACCCCTGGGACATGCTCAACCCCAAAAATAGCC	4363
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Qy	361	AlaAspGlyLeuValAlaValPheProValValArgGlyThrProLysAspSerCysSer	380
Db	5087	GCCGATGGGCTTGTGGCTGTGTGTTCCTCGGTGGTGGGGACCCCAAGGACAGTGTCTCC	5146
Qy	381	TyrLeuCysSerHisThrAlaAsnArgSerLysPheSerIleAlaAspGluAspAlaArg	400
Db	5147	TACCTGTGCTCACACAGCAACAGGTCCAACTTCAGCTCCGGATGAAGACGACGCGG	5206
Qy	401	GlnAsnProTyrProValLysAlaMetGluValValAsnSerGlySerGluValIleTyr	420
Db	5207	CAGAACCCCTTAACCAAGGAGGCGCATGAGAGTGTCAACACGGCTCTGAGGTCTGATC	5266
Qy	421	SerAsnGlyProGlyLeuLeuValIleAspCysAlaSerLeuGlnIleCysArgArgLeu	440
Db	5267	AGCATATGGCGGGCCCTCTTGTATGACTGTGGCTCCCTGAGAGATCTGCAGCGGCTG	5326
Qy	441	GluProTyrMetAlaProSerMetValThrSerValValCysSerSerGluLysArgGly	460
Db	5327	GAGCCCTACATGCCCCCTTCATGTGTTACGTCAAGTGTGTGTGCAGCTCTGAGGGCAGAGGG	5386
Qy	461	GluGlnValValTyrCysLeuAspAspLysAlaAsnSerLeuValMetTyrHisSerThr	480
Db	5387	GAGAGAGTCTCTGTGCTCGATGATGACAAAGCCAACTCTTGGATGATGTACCACTCCAC	5446
Qy	481	ThrTyrGlnLeuCysAlaArgTyrPheCysGlyValProSerProLeuArgAspMetPhe	500
Db	5447	ACCTACCAAGCTGTGTGCCGGAATCTTGTGGGGGTCCCAAGCCCCCTCAGAGACATGTTT	5506
Qy	501	ProValArgProLeuAspThrGluProProAlaAlaSerHisThrAlaAsnProLysVal	520
Db	5507	CCCGTGGGGCCCTTGGACAGGAACCCCCGGACGACGACACACGCGGCAACCCAAAGGTG	5566

QY 521 ProGluGlyAspSerIleAlaAspValSerIleMetTyrSerGluGluLeuGlyThrGln 540
 Db 5567 CCGAGGGGGAGCTCCATCCGAGCGGAGCATCATGATGAGGAGCTGGGACCCAG 5626
 QY 541 IleLeuIleHisGlnGluSerLeuThrAspTyrCysSerMetSerSerTyrSerSerSer 560
 Db 5627 ATCCGTATCCACAGGAATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 5686
 QY 561 ProProArgGlnAlaAlaArgSerProSerSerLeuProSerSerProAlaSerSerSer 580
 Db 5687 CCACCCCGCAGGCTCCGAGGTCCTCCCAAGCTCCCAAGCTCCCAAGCTCCCAAGCTCC 5746
 QY 581 SerValProPheSerThrAspCysGluAspSerAspMetLeuHisThrProGluAlaAla 600
 Db 5747 AGTGTGCTTTCTCCACCGACTGCGAGGACTGAGCATGCTACATAGCCCGGAGCTGCC 5806
 QY 601 SerAspArgSerGluHisAspLeuThrProMetAspGlyGluThrPheSerGlnHisLeu 620
 Db 5807 TCCGACAGGCTGAGCATGACCTGACCCCATGAGCGGAGACCTTCAGCCACGACCTG 5866
 QY 621 GlnAlaValIleLeuValAlaValArgAspLeuIleThrValProArgArgGlyValAsp 640
 Db 5867 CAGGCCGTGAAGATCTCCGCTCGAGAGCTCATTTGGGTCCCGAGCGCGGTGGAGAT 5926
 QY 641 ValIleValIleGlyLeuGluLysAspSerGluAlaGlnArgGlyArgValIleAlaVal 660
 Db 5927 GTTATCGTCATTGGCTGAGAGAGATTCTGGCGGCCAGCGGCGGAGTATTCGCCGTC 5986
 QY 661 LeuLysValAlaArgGluLeuThrProHisGlyValLeuValAlaAlaValAlaLys 680
 Db 5987 TTAAAGCCCGAGAGCTGACTCCGATGGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTG 6046
 QY 681 AspThrValValCysThrPheGluAsnGluAsnThrGluTyrCysLeuAlaValIleThrArg 700
 Db 6047 GACACTGTTGTGTGACCTTTGAAAATGAAAACAGAGTGTGTGCTGTGCTGTGAGG 6106
 QY 701 GlyTyrGlyValAlaArgGluPheAspIlePheTyrGlnSerTyrGluGluLeuGlyArgLeu 720
 Db 6107 GGCTGGGGCGCCAGGAGTTCGACATTTTCTACAGTCTTCAGAGAGCTGGCGGCTG 6166
 QY 721 GluAlaCysThrArgLysArgArg 728
 Db 6167 GAGGCTTGCACTGCGAAGAGAG 6190

RESULT 3
 US-10-132-382-1
 ; Sequence 1, Application US/10132382
 ; Publication No. US20030045699A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WEISS, BERTRAM
 ; TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROIDS
 ; FILE REFERENCE: SCH-1811
 ; CURRENT APPLICATION NUMBER: US/10/132,382
 ; CURRENT FILING DATE: 2002-04-26
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 7093
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-132-382-1

Alignment Scores:
 Pred. No.: 0 Length: 7093
 Score: 3579.50 Matches: 688
 Percent Similarity: 94.51% Conservatve: 0
 Best Local Similarity: 94.51% Mismatches: 1
 Query Match: 93.66% Indels: 39
 DB: 15 Gaps: 1

QY 1 MetLeuArgHisLeuAlaGlnAlaThrAspAlaMetLysAsnPheSerGluPheArgGlnGlu 20
 Db 4202 ATGTGAGGACACCTGGCGGCGCCAGAGCATCATGATGAGGAGCTTCGAGTTCGCGAGGAG 4261
 QY 21 AlaSerMetLeuHisAlaLeuGlnHisProCysIleValAlaLeuIleGlyLeuSerIle 40
 Db 4262 GCGAGCATGCTGCAGCGGCTGCAGACACCTGTGATGCTGCGCTCATTCGCGCATCAGCATC 4321
 QY 41 HisProLeuCysPheAlaLeuGluLeuAlaProLeuSerSerLeuAsnThrValLeuSer 60
 Db 4322 CACCGCTCTCTTGGCTGTGAGACTGCGCGCTCAGAGCTTCAACACCGTGTGCTCC 4381
 QY 61 GluAlaAlaArgAspSerPheIleProLeuGlyHisMetLeuThrGlnLysIleAla 80
 Db 4382 GAGAAAGCCAGATTCCTCTTATATCCCTGGAGACATGCTTCAACCCAAATAAGCC 4441
 QY 4442 TACCGAGTGGCTGGCGCTGGCTTACCTGACAGAAACATCATCTTCTGTGACCTG 4501
 QY 101 LysSerAspAsnIleLeuValIleThrSerLeuAspValIleGluHisIleAsnIleLysLeu 120
 Db 4502 AAGTGCAGACATTCGT 4561
 QY 121 SerAspTyrGlyIleSerArgLysPheHisGlnGlyAlaLeuGlyValGluGlyThr 140
 Db 4562 TCTGACTACGGATTTTGAGGACATTCATCATAGAGGCGCTTACGGCTGAGGCGACT 4621
 QY 141 ProGlyTyrGlnAlaProGluIleArgProArgIleValIleThrAspGlyLysValAspMet 160
 Db 4622 CCGGCTACAGGCGCCCGAGAGTACAGGCTTCGCTGTATATATATATATATATATATATAT 4681
 QY 161 PheSerTyrGlyMetValLeuTyrGluLeuLeuSerGlyGlnAspProAlaLeuGlyHis 180
 Db 4682 TTCTCTATGAAATGT 4741
 QY 181 HisGlnLeuGlnIleAlaLysLysLeuSerLysGlyIleArgProValLeuGlyGlnPro 200
 Db 4742 CACCGCTCCAGATTTGCGAAGATTCCTTCCAGGCGCTTCGCGGCTTCGCGGCGCGCG 4801
 QY 201 GluGluValAlaGlnPheArgSerLeuGlyAlaLeuMetGluCysThrAspThrLysPro 220
 Db 4802 GAGAAAGTGCAGTTCGCGGCTGCGAGCGCTCATATGAGAGTGTGTGTGTGTGTGTGTGTGT 4861
 QY 221 GluLysArgProLeuAlaLeuSerValIleSerGlnMetLysAspProThrPheAlaThr 240
 Db 4862 GAGAAAGCGACCGCTGGCTGT 4921
 QY 241 PheMetTyrGluLeuCysCysGlyLysGlnThrAlaPhePheSerSerGlnGlyGlnGlu 260
 Db 4922 TTCTATGTGAATCTGT 4981
 QY 261 TyrThrValAlaPheThrAspGlyLysGlnGluSerArgAsnTyrThrValAlaAsnThr 280
 Db 4982 TACACCGGT 5041
 QY 281 GluLysGlyLeuMetGluValAlaArgMetCysCysProGlyMetLysValSerCysGln 300
 Db 5042 GAGAAAGGCTTCATGAGGTGCGAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5101
 QY 301 LeuGlnValAlaGlnArgSerLeuThrThrAlaThrGluAspGlnLysIleTyrIleTyrThr 320
 Db 5102 CTCGAGTCCAGAGATCCCTGTGTGACAGCCACCGAG----- 5137
 QY 321 LeuLysGlyMetCysProLeuAsnThrProGlnGlnAlaLeuAspThrProAlaValAla 340
 Db 5137 ----- 5137
 QY 341 ThrCysPheLeuAlaValProValIleLysAsnSerTyrLeuValLeuAlaGlyLeu 360
 Db 5138 -----AATTCCTACTGT 5164
 QY 361 AlaAspGlyLeuValAlaValPheProValValArgGlyThrProLysAspSerCysSer 380

Db 5165 GCCGATGGCTTGTGCTGTTTCCCGTGGTGGGCGACCCCAAGACAGCTGCTCC 5224
 QY 381 TyrLeuCySerHisThrAlaAsnArgSerLysPheSerIleAlaAspGluAspAlaArg 400
 Db 5225 TACCTGTGCTCACACACAGCAGGTCCAGTTCAGCATGCGAGTGAAGACGCAAG 5284
 QY 401 GluAsnProTyrProValIysAlaMetGluValIysAlaSerGlySerGluValTyrTyr 420
 Db 5285 CAGAACCCCTACCCAGTGAAGGCCATGAGGTGTGCAACAGGGCTCTGAGGCTGGTAC 5344
 QY 421 SerAsnGlyProGlyLeuLeuValIleAspCysAlaSerLeuGluIleCysArgArgLeu 440
 Db 5345 AGCAATGGCGGGGCTCTTGTGATCGACTGTGCTCCCGAGATCTGACGGCGGCTG 5404
 QY 441 GluProTyrMetAlaProSerMetValThrSerValValCysSerSerGluGlyValGly 460
 Db 5405 GAGCCTACATGGCCCCCTCCATGGTTAGTCACTGATGTCAGTCTGAGGGCAGAGG 5464
 QY 461 GluGluValValTyrCysLeuAspAspLysAlaAsnSerLeuValMetTyrHisSerThr 480
 Db 5465 GAGGAGTGTGCTGTGCTGATGACAGGCCAATCTCTGTGATGTACCTCACTCCACC 5524
 QY 481 ThrTyrGlnLeuCysAlaArgTyrPheCysGlyValProSerProLeuArgAspMetPhe 500
 Db 5525 ACCTACACAGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5584
 QY 501 ProValArgProLeuAspThrGluProProAlaAlaSerHisThrAlaAsnProVal 520
 Db 5585 CCGGTGGGCCCCCTTGGACACGGAAACCCCGGACGACCCACAGGCCAACCAAGGTTG 5644
 QY 521 ProGluGlyAspSerIleAlaAspValSerIleMetTyrSerGluGluLeuGlyThrGln 540
 Db 5645 CCGAAGGGGAGCTCCATCGCGAGCGAGCATCATGTACAGTGAAGAGCTGGCAGCCAG 5704
 QY 541 IleLeuIleHisGlnGlnSerLeuThrAspTyrCysSerMetSerSerTyrSerSerSer 560
 Db 5705 ATCTGATCCACAGGAATCACTCACTGCTACATGCTCCATGCTCTCTACTCTCTATCC 5764
 QY 561 ProProArgGlnAlaAlaArgSerProSerSerLeuProSerSerProAlaSerSerSer 580
 Db 5765 CCACCCCGCAGGCTGCCAGGTCCCTCCATAGCCCTCCACACTCCCAAGAAATCTTCC 5824
 QY 581 SerValProPheSerThrAspCysGluAspSerAspValLeuHisThrProGlyAlaAla 600
 Db 5825 AGTGTGCCCTTCTCCACCGCATCGCAGGACCTCAGCATGCTACATACGCCCGGTGCTGCC 5884
 QY 601 SerAspArgSerGluHisAspLeuThrProMetAspGlyGluThrPheSerGlnHisLeu 620
 Db 5885 TCCGACAGTCTGACATGATCTGACCCCATGACGGGGAGACCTTCAGCCAGCACTTG 5944
 QY 621 GlnAlaValIysIleLeuAlaValArgAspLeuIleTyrValProArgArgGlyIleAsp 640
 Db 5945 CAGGCCGTGAAGATCTCCGCTCAGAGACCTCATTTGGGTCCCAAGCGGGGGAGAT 6004
 QY 641 ValIleValIleGlyLeuGlnLysAspSerGluAlaGlnArgGlyArgValIleAlaVal 660
 Db 6005 GTTATGCTATTGGCTGGAGAGATTCGTGGCGGCCAGCGGCGAGGTATGCGCTC 6064
 QY 661 LeuLysAlaArgGluLeuThrProHisGlyValLeuValAspAlaAlaValAlaLys 680
 Db 6065 TTTAAAGCCCGAGAGCTGACTCCGATGGGGGTGCTGTGATGCTGCGGTGTGGCAAG 6124
 QY 681 AspThrValValCysThrPheGluAsnGluAsnThrGluTyrCysLeuAlaValTyrArg 700
 Db 6125 GACACTGTTGTGTGACCTTTGAAAATGAAAACAGAGGTGTGCTGGCGTGTGAGG 6184
 QY 701 GlyTyrGlyAlaArgGluPheAspIlePheTyrGlnSerTyrGluGluLeuGlyArgLeu 720
 Db 6185 GGCTGGGGCGCAGAGGAGTTGACATTTTCTACACAGTCTCTACAGAGAGCTGGCGGCTG 6244
 QY 721 GluAlaCysThrArgLysArgArg 728

Db 6245 GAGGCTTGCACTCGCAGAGAGAG 6268
 RESULT 4
 US-10-132-382-7
 / Sequence 7, Application US/10132382
 / Publication No. US20030046599A1
 / GENERAL INFORMATION:
 / APPLICANT: WEISS, BERTRAM
 / TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROIDS
 / FILE REFERENCE: SCH-1811
 / CURRENT APPLICATION NUMBER: US/10/132,382
 / NUMBER OF FILING DATE: 2002-04-26
 / NUMBER OF SEQ ID NOS: 26
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO 7
 / LENGTH: 7229
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 US-10-132-382-7
 Alignment Scores:
 Pred. No.: 0 Length: 7229
 Score: 3579.50 Matches: 688
 Percent Similarity: 94.51% Conservative: 0
 Best Local Similarity: 94.51% Mismatches: 1
 Query Match: 93.66% Indels: 39
 DB: 15 Gaps: 1
 US-09-836-392-21 (1-728) x US-10-132-382-7 (1-7229)
 QY 1 MetLeuArgHisLeuArgAlaThrAspAlaMetLysAsnPheSerGluPheArgGlnGlu 20
 Db 4338 ATGTGAGGACCTGGGGGCCACCGATGCAATGAGAACTTCCCGAGTCCGCGCAGAG 4397
 QY 21 AlaSerMetLeuHisAlaLeuGlnHisProCysIleValAlaLeuIleGlyIleSerIle 40
 Db 4398 GCGACGATGCTGACGCGCTGACACACCCTCGATCGTGGCGCTCATGCGCATGAGCATC 4457
 QY 41 HisProLeuCysPheAlaLeuGluLeuAlaProLeuSerSerLeuAsnThrValLeuSer 60
 Db 4458 CACCGGCTGCTGCTGCGCTGAGACTGCGCGCGCTCAGACGCTCAACACCGTGTCTCC 4517
 QY 61 GluAsnAlaArgAspSerSerPheIleProLeuGlyHisMetLeuThrGlnLysIleAla 80
 Db 4518 GAGAACCGCAGAGATCTCTCTTAAACCCCTGGGACACATGCTCACCAAAAATAAGCC 4577
 QY 81 TyrGlnIleAlaSerGlyLeuAlaTyrLeuHisLysLysAsnIleIlePheCysAspLeu 100
 Db 4578 TACGAGATCGCTCGGGCTGCGCTTACTCTGACACAGAAACATCATCTTCTGTGACCTG 4637
 QY 101 LysSerAspAsnIleLeuValTyrSerLeuAspValIysGluHisIleAsnIleLysLeu 120
 Db 4638 AAGTCGACCAATTCGTGTGTGCTGCTCCCTGACCTCAAGAGACATCAACATCAAGCTA 4697
 QY 121 SerAspTyrGlyIleSerArgGlnSerPheHisGlnGlyAlaLeuGlyValGlnGlyThr 140
 Db 4698 TCTGACTGCGGATTTGAGGCACTTCTCAATAGGCGCCCTTAGCGCTGAGGGCACT 4757
 QY 141 ProGlyTyrGlnAlaProGluIleArgProArgIleValTyrAspGluLysValAspMet 160
 Db 4758 CTGGCTACAGGCGCCAGAGATCAGGCTCGCATTTGATGATGAGAGGTAGATATG 4817
 QY 161 PheSerTyrGlyMetValLeuTyrGluLeuLeuSerGlyGlnArgProAlaLeuGlyHis 180
 Db 4818 TTCTCTATGGAATGAGTCTCTACAGTCTCTGTCAGAGACAGCGCCCTGCACTGGGCGAC 4877
 QY 181 HisGlnLeuGlnIleAlaLysLysLeuSerLysGlyIleArgProValIleuGlyGlnPro 200
 Db 4878 CACCAAGCTCCAGATTTGCCAAGAGCTCTCCAAAGGCAATCCGCCGGTCTGGGCGAGCG 4937
 QY 201 GluGluValGlnPheArgArgLeuGlnAlaLeuMetMetLysCysTyrPhePheTyrPro 220
 Db 4938 GAGGAAGTGACGTTCCGGCAGCTGACAGCGCTCATGATGAGTGTGGGCACTAAGCCA 4997

QY	22	GLUYSARGPROLEUALALEUSERVAIALSEGIMETLYASPPROTHPHEALATHR	240
Db	4998	GAGAACCAACCGCTGACCGCTCTCCGTGGTGAACCAAGTAAGAACCCAGCTTTTCCACC	5057
QY	241	PHMETYRGILUEUCYSCYSGILVYSGINTHRAIPHESESERDINGILGU	260
Db	5058	TTCAAGTATGAACGTGTGCTGGAGACAGACGCTTCTTTCATCCAGGGCCAGAG	5117
QY	261	TYTTRVAIVAIAPHETRASPGLVLYSGILGUSERYGAANTYTHRAIYALASNTHR	280
Db	5118	TACACCGTGCGTATTTTGGGATGAAAAAGAGATCCAGAACTACACGGTGTGAACCA	5177
QY	281	GIULYSGILYUEMETGIUVAIGIARYMETCYSCYAFROGILMETIYVAISERCYSGIN	300
Db	5178	GAGAAAGGGCTCATGAGAGGTCAAGAGATGCTGCCCTCGAGTAGAGGTGAGCTGCAG	5237
QY	301	LEUGINVAIGIARYSERLEUTRTHAIAETHGUAPOGILNLYETRIYENYTHR	320
Db	5238	CTCCAGGTCCAAAGATCCCTGTGACACGACCCAG-----	5273
QY	321	LEULYSGILMETCYSPROLEUASNTHPROGILGNALALEUASNTHPROALVAIVAI	340
Db	5273	-----	5273
QY	341	THRCYSPHELEUALAIVAIPROVAIIELUYELYSANSEYTRILEUVAILEUAGIYEU	360
Db	5274	-----AAITCTCACTGTGCTTACGGGGCTTC	5300
QY	361	ALASPGLYUEUVALAIVAIAPHEPROVAIVAIARGIYTHPROLYASPSERCYSSER	380
Db	5301	GCCGATGGGCTTGTTGGCTGTATTTCCCGTGGTGGGGGACCCCAAGAGACGCTGCCTC	5360
QY	381	TYREUCYSSERHISTHRAIASNARSERYSPHESERIELEIASPILUNSPALARG	400
Db	5361	TACCTGTGTGTACACACAGCCAAAGGTCCAAATTGACATCCGGATATAAACACCAAG	5420
QY	401	GIAPSNPROTYPROVALIYVAIAMEGILUVAIVAIASNSERCYSGERGIUVAITPTYR	420
Db	5421	CAGAACCCCTACCCAGTAGAAGCATGAGAGTGTGTCAACGGCGCTCATAGCTCGAGTAC	5480
QY	421	SERASNGIYPROGIYUEUENVAIIIEASPOCYASLASERENDIULECYARGRYEU	440
Db	5481	AGGAAGGGCCGGCGCTCTTGTCTATGATGATGCTGTGCTCCCTGGAAGTCTGACGGGCTG	5540
QY	441	GIUPROTYMETALPROSEMETVAITHSERVAIACYSSERSEGIUVAIRGILY	460
Db	5541	GAGCCCTCATGAGCCCCCTCATGGTATACGTCAGTCTGTGCAAGCTCATGAGGCGAGAAGG	5600
QY	461	GIUGIIVAIIVAITPTCYLEUASAPPLYAIIASNSERLEUVAIEMETYTHIASERTHR	480
Db	5601	GAGAGAGTGTCTGTGCTGTGAGTGAACAAGCCAACTCTGTGATATGACATCTCCAC	5660
QY	481	THYTRGILUEUCYALARYTYRPHCYSGILYVAIPROSERPROLEUARGAPMETHE	500
Db	5661	ACCTACCACTGTGTGGCCCGGACTTGTGCGGGTCCCGAGCCCTCCAGGAGCATGTTT	5720
QY	501	PROVALARGPROLEUASPTHRGIUPROPROALIASERIETHRIIASNPROCYVAL	520
Db	5721	CCCGTGGCGCTTTGGACACGGAACCCCGGACCGACACACGCGCAACCAAGATG	5780
QY	521	PROGILUVAIPSERIELEIASPVASERILEMETYSEGIUENUGILYTHRGIN	540
Db	5781	CCGAGAGGGAGCTTCATGCGGACGTGACATCATATGACATGAGAGAGCTGGACAGAG	5840
QY	541	ILEUENILEHIGILUSERLEUTHASPTCYCYSSERMETSESEYTYSESSER	560
Db	5841	ATCTGATCCACAGAGATCACTCACTGACTACATGCTCATGCTCTCACTCTCACTCC	5900
QY	561	PROPROARGILNALIASERPROSESERLEUAPROSESERPROLASERSESER	580
Db	5901	CCACCCCGGACAGCTGCAGATCCCGCTCAAGCTCCCAAGCTCCCAAGAGTTCTTC	5960

QY	581	serValpRopPheSerThrAspCySGIAspSerAspMetLeuHisThrProGlyValAla	600
Db	5861	AGTGTGCTTTCTTCCACGCACTGGAGAGACTCAGACACTGCTTAATACGCCGGTGTGCC	6020
QY	601	SeRAspArgSerGlnHisAspLeuThrProMetAspGlyGlnThrPheSerGlnHisLeu	620
Db	6021	TCCGACAGGCTGTGAGCTGACCTGACCTGACCCCATGGACGGGAGAGCTTCACCCGACACTG	6080
QY	621	GlnHisValIleValIleLeuHisValArgAspLeuIleThrValProArgArgGlyGlyAsp	640
Db	6081	CAGGCCCGGAAGATCTCCGCGCTGAGAGACTCATTTGGGTCTCCCAAGCGCGGGAGGAT	6140
QY	641	ValIleValIleGlyLeuGlnIleAspSerGlnHisAspGlnArgGlyArgValIleHisVal	660
Db	6141	GTTATCGTCATTTGSCCTCGAGAGAGATTTCTGGGGCCACGGGGGCGGAGTCATTTGCCCTC	6200
QY	661	LeuHisValArgGlnLeuThrProHisGlyValLeuValAspAlaHisValHisValHis	680
Db	6201	TTAAAGCCCGAGAGCTGACCTCCGCACTGGGTCTGTGTGATGCTGTCCGTGGGCAAG	6260
QY	681	AspThrValValCysThrPheGlnHisGlnHisAsnThrGlnThrCysLeuHisValAspArg	700
Db	6261	GACACTGTGTGTGTGCACTTTGAAAAAGAAACACAGAGTGTGTGCTGTGCCCTGTGAGG	6320
QY	701	GlyThrGlyAlaArgGlnPheAspIlePheThrGlnSerTyrglnGlnLeuGlyArgLeu	720
Db	6321	GGCTGGGGCGCCAGAGGAGTTGCACTTTCTTACAGACTCTAAGAGAGAGCTGGGGCGGCTG	6380
QY	721	GlnHisValCysThrArgIleArgIleArgArg 728	
Db	6381	GAGGCTTGCACTCGCAAGAGAGAG 6404	
RESULT 5			
US-10-132-382-3			
Sequence 3, Application US/10132382			
Publication No. US20030045699A1			
GENERAL INFORMATION:			
APPLICANT: WEISS, BERTRAM			
TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROLS			
FILE REFERENCE: SCH-1811			
CURRENT APPLICATION NUMBER: US/10/132,382			
CURRENT FILING DATE: 2002-04-26			
NUMBER OF SEQ ID NOS: 26			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 3			
LENGTH: 7307			
TYPE: DNA			
ORGANISM: Homo sapiens			
US-10-132-382-3			
Alignment Scores:			
Pred. No.: 0 Length: 7307			
Score: 3579.50 Matches: 688			
Percent Similarity: 94.51% Conservative: 0			
Best Local Similarity: 94.51% Mismatches: 1			
Query Match: 93.66% Indels: 39			
DB: 15 Gaps: 1			
US-09-836-392-21 (1-728) x US-10-132-382-3 (1-7307)			
QY	1	MetLeuArgHisLeuArgAlaThrAspAlaMetLysAsnPheSerGlnPheArgGlnGln	20
Db	4416	ATGCTGAGGACCTGCGGGCCACCGCATGCCATGAAGAACTTCTCGAGTTCCGGCAGAG	4475
QY	21	AlaSerMetLeuHisAlaLeuGlnHisProCysIleValHisLeuIleGlyIleSerIle	40
Db	4476	GCCAGCAGCTGACGCGCTGACACACCCCTGCATCTGTGGGCTGCATCGGCATGAGATC	4535
QY	41	HisProLeuCysPheAlaLeuGlnLeuAlaProLeuSerSerLeuAsnThrValLeuSer	60
Db	4536	CACCCGCTCTCTCCGCTCGAGCTCGCCGCGCTCAGACGCTCAACACCGTGTCTCTCC	4595
QY	61	GlnAsnAlaArgAspSerSerPheIleProLeuGlnHisMetLeuThrGlnLysIleAla	80

Db		4595	GAGAAAGCCAGGATTTCTTCTTATACCTGGGACATGCTTCAACCCAAAAATTACCC	4655
Oy		81	TYGInIleAlaSerGlyLeuAlaIleuAlaIleuHisLeuSerAsnIleIlePheCysAspLeu	100
Db		4656	TACCAATGCTGCTCGGGCTGGCCCTACTGCAAGAAAACATCATCTTCTGTGACCTG	4715
Oy		101	IleSerAspAsnIleLeuValTyrSerLeuAspValIleGluHisIleAsnIleLeuLeu	120
Db		4716	AATTCGGAACAACATTCGTGATGGTCCCTTGACCTCAAGAGCAATCAACATCAAGCTA	4775
Oy		121	SerAspTyrGlyIleSerArgGlnSerPheHisGluValAlaLeuGlyValGluGlyThr	140
Db		4776	TCTGACTAAGGGATTTCCAGGGACATTCATCAATAGGGCCCTTAAGCCTGGAGGCACT	4835
Oy		141	ProGlyTyrGlnAlaProGluIleArgProArgIleValTyrAspGluSerValAspMet	160
Db		4836	CCGGGTACAGAGCCCAAGATCAAGGCTTCGCTATGATATGATAGAAAGGTAAATATG	4895
Oy		161	PheSerTyrGlyMetValIleuTyrGluLeuLeuSerGlyValGlnArgProAlaLeuGlyHis	180
Db		4895	TTCTCTTAATGAAATGGTGTCTTACAGATGTGTGTGCAGAAAGGCCCTCACTGGGCAAC	4955
Oy		181	HisGlnLeuGlnIleAlaValLeuSerLeuSerIleGlyIleArgProValIleuGlyGlnPro	200
Db		4956	CACCACTCCAAATGGCCAAAGAGTGTCCAAAGGCAATCCGGCTTCTGGGCAAGCCG	5015
Oy		201	GluGluValGlnPheArgArgLeuGlnAlaLeuMetGluGlyArgThrAspThrIlePro	220
Db		5016	GAGAAAGTCAAGTCCGGGCACTGCAAGGCTCATGTATGATGGATGGGACACTAAGCA	5075
Oy		221	GluIleArgProLeuAlaLeuSerValIleSerGlnMetLeuSerAspProThrPheAlaThr	240
Db		5076	GAGAAAGCAACCGCTGGCCCTGTGCGTGGTGTAGCCAAATGAAGAACCCGACTTTTGCACC	5135
Oy		241	PheMetTyrGluLeuLeuCysCysGlyValGluGlnThrAlaPhePheSerSerGlnGlyGlnIu	260
Db		5136	TTCATATTAAGACTGTGCTGTGGAAAGACACACCTTCTTCATCCAGGCGCAAGAG	5195
Oy		261	TyrThrValValPheTyrAspGlyValGluGluLeuSerArgSerIleThrValValAsnThr	280
Db		5196	TACACCTGTGTGTTTGGGATGGAAATAGAGATCCAGAACTACACGGTGGTGAACACA	5255
Oy		281	GluIleGlyLeuMetGluValGlnArgMetCysCysProGlyMetLeuValSerCysGln	300
Db		5256	GAGAAAGGCTCATGAGAGTGCAGAGATGTGCTGCCCTGGATGAGAGTGAAGTGCAGCAG	5315
Oy		301	LeuGlnValGlnArgSerLeuTyrThrAlaThrGluAspGlnIleIleTyrIleTyrThr	320
Db		5316	CTCCAGGTCAGAGATCCCTGTGGACCAACCCAG-----	5351
Oy		321	LeuIleGlyMetCysProLeuAsnThrProGlnAlaLeuAspThrProAlaValVal	340
Db		5351	-----	5351
Oy		341	ThrCysPheLeuAlaValProValIleLeuSerAsnSerTyrIleuValIleuAlaGlyLeu	360
Db		5352	-----AATTCCTAAGCTGATTTACGGGCTCC	5378
Oy		361	AlaAspGlyLeuValAlaValPheProValValArgGlyThrProIleSerAspCysSer	380
Db		5379	GCCGATGGGCTTGTGGCTGTGTTTCCGTGTGCGGGGCAACCCAAAGACAGCTGCTCC	5438
Oy		381	TyrLeuCysSerHisThrAlaAsnArgSerIlePheSerIleAlaAspGluAspAlaArg	400
Db		5439	TACCTGTGCTCACACAGCCAAAGGTCCAAAGTTCAGATCCGGATGAAACACACAGG	5498
Oy		401	GlnAsnProTyrProValIleAlaMetGluValValAsnSerGlySerGluValTyrTyr	420
Db		5499	CAGAAACCTCAACCACTGAAGCCATGGAAGTGTCAACAGCGCTCTAGAGTGTGATAC	5558
Oy		421	SerAsnGlyProGlyLeuLeuValIleAspCysAlaSerLeuGluIleCysArgArgLeu	440

Db	5559	AGCAATGGGCGGGCCCTCTGTATGACACTGTGCTCCCTCGAGAGATCTGACGGCGGCTG	5618
Qy	441	GIueProTyMeTalAProSeMeValThiSeValValCySeSeSerGIuGIYArgGIY	460
Db	5619	GAGCCCTTCATGGCCCCCTCCATGGTAAAGCTGCTGTGTACACTCTGAGGGCAGAGGG	5678
Qy	461	GIuGIuValValTTPCySLeuAspAspValAsmSerLeuValMeCTYrHisSeSerThr	480
Db	5679	GAGAGAGGTGCTGTGTGTGTGACAGACAGGCCCACTCTTGAGAGTACACTCCACCC	5738
Qy	481	ThTYrGIuLeuCySAIaArgTYrPheCySeGIYValProSeProLeuArgAspMePhe	500
Db	5739	ACCTAACCAAGCTGTGTGGCCGGTATTCTTGCGGGGTCTCCAGGCCCTCTCAGGACATGTTT	5798
Qy	501	ProValAArgProLeuAspThrGIuProProAlAlaSerHisThrAlaAsnProLyVal	520
Db	5799	CCCGGCGGGCCCTTGGACACGGAAACCCCGGACCCAGCCACAGGGCCAAACCCAAAGGTG	5858
Qy	521	ProGIuGIYAspSerIleAlaAspValSerIleMeTYrSeSerGIuGIuLeuGIYThGIu	540
Db	5859	CCTGAGGGGAGCTCATTCGCCGAGTGAAGCATCATGTACAGTAGAGAGAGCTGGGACCCAG	5918
Qy	541	IleuIleHisGIuGIuSerLeuThrAspTYrCySeSerMeSeSerTYrSeSeSer	560
Db	5919	ATCTGATCCACACGAGATCATCATGACACTACGCTCCATGTCTCTCTCATCTCCATACC	5978
Qy	561	ProProAlArgGIuAlAlaArgSeProSeSerLeuProAsSerProAlaSerSeSer	580
Db	5979	CCACCCGCGCAGGCTGCCAGGTCTCCCTCAAGCTCCCGACCTCCCAAGCATTTCTTCC	6038
Qy	581	SeValAProPheSerThrAspCyGIuAspSerAspMeLeuHisThrProGIYAlAla	600
Db	6039	AGTGAGCTTCTCTCCACGCACTGCGAGGAGACTCAGACATGCTACATAGCCCGGCGTGGCC	6098
Qy	601	SeAspAspAspSerGIuHisAspLeuThrProMeAspGIuGIuThrPheSerGIuHisLeu	620
Db	6099	TCCAGCAGGTCTGACATGACTGATACCCCACTGGACGCGGAGACTTCAGCCAGCACCCTG	6158
Qy	621	GIuAlaValValIleLeuAlaValAlaArgAspLeuIleTPValProArgArgGIYGIYAsp	640
Db	6159	CAGGCGCGAGAGATCTCTCGCGCTCAGAGACCTCATTTGGGTCCCCCAGCGCGGTGGAGAT	6218
Qy	661	ValIleValIleGIYLeuGIuLyAspSerGIuAlaGIuArgGIYAlaValIleAlaVal	660
Db	6219	GTTATCGCATTTGCCCTGGAGAAAGATTTGGCGCCCAAGCGGGCGCAGCATTTGCCGTC	6278
Qy	661	LeuValAlaArgGIuLeuThrProHisGIYValLeuValAspAlaAlaValAlaVal	680
Db	6279	TTAAAGCGCCAGAGAGCTGACTCCGCAAGGGGTCTGTGTGATGCTGCGGTGTGGCAAAG	6338
Qy	661	AspThrValValIYrThrPheGIuAsnGIuAsnThrGIuTPCySeuAlaValITPArg	700
Db	6339	GACACTGTGTGTGACACTTTGAAAGAAACAGACAGTGTGCTCGCGCGCTGTGAGG	6398
Qy	701	GIYTPGIYAlaArgGIuPheAspIlePheTYrGIuSerTYrGIuGIuLeuGIYArgLeu	720
Db	6399	GCGTGGGGCGCCAGAGAGATTGACATTTTCTTACACAGTCTTACGAGGAGCTGGCGCGGCTG	6458
Qy	721	GIuAlaCyThrArgLyAspArg	728
Db	6459	GAGGCTTGCATCTCGCAAGAGAGG	6482

RESULT 6

US-10-094-749-50

Sequence 50, Application US/10094749

Publication No. US20030219741A1

GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO

APPLICANT: SUGIYAMA, TOMOYASU

APPLICANT: OTSUKI, TETSUJI

APPLICANT: MAYKAMATSU, AI

APPLICANT: SATO, HIROYUKI

APPLICANT: ISHII, SHIZUKO

APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUKIO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOTIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOKYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 08435/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50
LENGTH: 3112
TYPE: DNA
ORGANISM: Homo sapiens
US-10-094-749-50

Alignment Scores:
Pred. No.: 0 Length: 3112
Score: 3225.00 Matches: 616
Percent Similarity: 99.84% Conservative: 0
Best Local Similarity: 99.84% Mismatches: 1
Query Match: 84.38% Indels: 1
DB: 13 Gaps: 0

US-09-836-392-21 (1-728) x US-10-094-749-50 (1-3112)

QY 112 VallyeGluHsielleanilleysleuseAepTYRGIYIleSerArgInserPheHis 131
DB 2 GTCAGAGAGACATCAACATCAAGCATGTGACTACGGGATTTCAGGCACTATTCAT 61
QY 132 GluGlyAlaLeuGlyValGluGlyThrProGlyTYRGINAlaProGluIleArgProArg 151
DB 62 GAGGGGCGCCCTAGCGCTGAGGAGGCACTCTGCTCCAGGCCCAAGATAGGCGCTCGC 121
QY 152 IleValTYRAspGluIleValAspMetPheSerTYRGIYMetValIleuTYRGIleuIleu 171
DB 122 ATTGTATATCATAGAAAGTAAATATGTTCTCTATGAAATGCTCTTACAGATTGCTG 181
QY 172 SerGlyGlnArgProAlaLeuGlyHisHisGlnLeuGlnIleAlaValSerLeuSerIys 191
DB 182 TCAGAGACAGCGCCCTGCACTGGGCCACACAGCTCCAGATTGCCAAGAAAGCTGTCCAG 241
QY 192 GlyIleArgProAlaLeuGlyGlnProGluGluValGlnPheArgArgLeuGlnAlaLeu 211
DB 242 GGCATCCGCCCGGTCTTGAGGACAGCCGAGAAAGTGCATTTCCGCCGACTGAGCGCTC 301
QY 212 MetMetGluCysTyrPheSerThrIleProGluIleArgProLeuAlaLeuSerValIleSer 231
DB 302 ATGATGAGAGTGTGGGACATAGCCAGAGAAAGCAAGCGCTGCGCTGTGAGTGGAGC 361
QY 232 GlnMetIleArgProThrPheAlaThrPheMetTYRGIleuIleuCysCysGlyIleGlnThr 251
DB 362 CAGATGAAGACCCGACTTTGGCACCTTCATGTATGAACCTGTGCTGTGGAAAGAGACA 421
QY 252 AlaPheSerSerArgGlnGlnGlnIleGlyIleValIlePheTYRAspGlyIleGlnGln 271
DB 422 GCCTTCTTCTCATCCAGAGCCAGAGTACACCGTGTGTTTGGGAAGAAAGAGAG 481
QY 272 SerArgAsnTYRThrValValAlaThrThrGlyIleuMetGluValGlnArgMetCys 291
DB 482 TCCAGGAACCTACAGCGGTGTGAACACAGAAAGGCGCTCATGAGAGTGCAGAGATGTGC 541

QY 292 CysProGlyMetIleValSerCysGlnLeuGlnValGlnArgSerIleuThrAlaThr 311
DB 542 TGCCCTGGAGTGAAGGTGAGGTGCACTCCAGCTCCAGATCCAGATCCCTGTGAGACAGCCACC 601
QY 312 GluAspGlnIleTYRleTYRThrLeuGlyMetCysProLeuSerThrProGln 331
DB 602 GAGACAGAAATCTACATCTACACCTCAAGGCAATGCGCCCTTAAACACACCCCA 661
QY 332 GlnAlaLeuAspThrProAlaValIleThrCysPheLeuAlaValProValIleIleIysIys 351
DB 662 CAGGCTTGATATCCAGCTGTGTGCACTGCTTTCGCGCTGTGTTATTAAGAG 721
QY 352 AsnSerTYRleuValIleuAlaGlyIleuAlaAspGlyIleuValAlaValPheProValIle 371
DB 722 AATTCCTACCTGTGCTTACGCGGCTTCGCGATGCGCTTGTGCTGTGTTCCCGTGG 781
QY 372 ArgGlyTYRProIleAspSerCysSerTYRleuCysSerHisThrAlaAsnArgSerIys 391
DB 782 CGGGGACCCCAAGAGACAGCTGCTCTACCTGTGCTCACACACAGCCACAGCTCCAG 841
QY 392 PheSerIleAlaAspGluAspAlaArgGlnAsnProIleProValIleMetGluVal 411
DB 842 TTCAGCATCGGAGTGAAGACGACGCGACAAACCTTACCACTGAAGGCCATGAGG 901
QY 412 ValAsnSerGlySerGluValTYRProIleSerAsnGlyProGlyIleuValIleAspCys 431
DB 902 GTCAACACAGGCTCTGAGTCTGTGTACAGAAAGGCGCGGCTCTGTGCATGCACTGT 961
QY 432 AlaSerLeuGluIleCysArgArgLeuGluProTYRMetAlaProSerMetValIleSer 451
DB 962 GCTTCCTCGAGATCTGAGGCGGCTGAGCCCTTACATGCCCCCTTCATGTTAGTGC 1021
QY 452 ValValCysSerSerGluGlyArgGlyGluValValTYRProCysLeuAspAlaVal 471
DB 1022 GTGCTGTCACTCTGAGGCGAGGAGGAGAGGTGCTGTGCTGTGATGACAAAGGC 1081
QY 472 AsnSerLeuValMetTYRHisSerThrTYRGIleuIleuCysAlaArgTYRPhleCysGly 491
DB 1082 AACTCTGTGATGATACACTCCACACCTTACAGCTGTGTGCGCGTACTTCTCGGG 1141
QY 492 ValProSerProLeuArgAspMetPheProValArgProLeuAspThrGluProProAla 511
DB 1142 GTCCCAAGCCCTTCAGGACATATTTCCGTGGGCGCTTGGACACAGAACCCCGGCA 1201
QY 512 AlaSerHisThrAlaAsnProIleValProGluIleAspSerIleAlaAspValSerIle 531
DB 1202 GCCACCCACACGGCCCAACCAAGGTGCTGAGGGGAGCTCCATCGCGGACGTGAGCATC 1261
QY 532 MetTYRserGluIleuGlyTYRGIleIleuIleHisGlnIleuSerLeuThrAspTYR 551
DB 1262 ATGTACAGTGAAGAGCTGGGACACGAAATCTGTATCCACAGAAATACATCATGACTAC 1321
QY 552 CysSerMetSerSerTYRserSerSerProProArgGlnAlaIleArgSerProSerSer 571
DB 1322 TGCTCCATGTCTCTTACTTCTCATCCACCCGCGGAGGCTGCAAGTCCCTCAAGC 1381
QY 572 LeuProSerSerProAlaSerSerSerSerValProPheSerThrAspCysGluAspSer 591
DB 1382 CTCCCACTCCCAAGAGTCTTCCAGTGTGCTTCTCCACGCACTCGAGAGACTCA 1441
QY 592 AspMetLeuHisThrProGlyAlaAlaSerAspArgSerGlnHisAspLeuThrProMet 611
DB 1442 GACATGTCAATACGCCCGGTGCTGCTCGACAGAGCTGAGCATGATGACCCCATG 1501
QY 612 AspGlyGluThrPheSerGlnHisLeuGlnAlaValIleValIleuAlaValArgAspLeu 631
DB 1502 GACGGGAGACCTTACGACACACCTGAGGCGCTGAGAGATCTGCGCTGACAGACTTC 1561
QY 632 IleTYRValProArgArgGlyIleAspValIleValIleGlyIleuGluIleAspSerGlu 651
DB 1562 ATTTGGTCCCAAGCGCGT-GAAGATTTATGCTATGTGGCTGGAAGAGATTCGAA 1620

QY 99 AspLeuYSerSerAspApnIleLeuValITPSeSerLeuAspValLySGuNH:ILASenIle 118
Db 12 GACCTGAAGTCGACCAACATCTCGTGTGTGCTCCCTTGACGTCAAGAGCAATCAATCAATC 71
QY 119 LysLeuSerAspTyTcGlyIleSerArgInserPheH:sgIuGlyAlaLeuGlyValGlu 138
Db 72 AAGCTATCTACTACCGGATTTCTGAGGCAAGTATTCCATGAAGGGGGCCCTTGGGTGGAG 131
QY 139 GlyTYhrProGlyTyTcGlnAlaProGluIleArgProArgIleValTYrAspGluLyVal 158
Db 132 GGCACCTCCTGGTACCACAGGCCCCAGAGATCAAGGCCCTCGCATGTATGATGAAGAGTA 191
QY 159 AsphePheSerTyTcGlyMetValLeuTyTcGluLeuSerGlyGlnArgProAlaLeu 178
Db 192 GATATGTCTTCCTTGAAATGAGTCCTTCAGATTGCTCTCAAGACACGCCCTCGCATG 251
QY 179 GlyHisIscGluLeuGlnIleAlaLybLybLeuSerLybGlyTLeArgProValLeuGly 198
Db 252 GGCACACACAGCTCCAGATTCGCCAAGAGCGTCCAAAGGCATCGGCCGCGTCTGGG 311
QY 199 GlnProGluIuValGlnPheArgArgLeuGlnAlaLeuMetGluCySerTyrAspThr 218

Alignment Scores:

Pred. No.: 4,91e-27 Length: 3052
 Score: 341.50 Matches: 111
 Percent Similarity: 48.35% Conservative: 80
 Best Local Similarity: 28.10% Mismatches: 150
 Query Match: 8.94% Indels: 55
 DB: 13 Gaps: 14

US-09-836-392-21 (1-728) x US-10-115-482-47 (1-3052)

QY 10 Alamelysanpserglu-----Phearglnglnualasermet 23
 DB 999 GCTGTGAAGATTTTAAATAACATACACTCAGGCTGTGTAAGACAGAGCTGGTG 1058
 QY 24 LeuhsalaleuGlnHisProCysIleValAlaleuilegylIleSerIleHisProleu 43
 DB 1059 CTTTGCCACCTCCACACCCCAAGTTTATCTTGTGTGAGCTGGAGTTCCCTCCCG 1118
 QY 44 CysPheAlaleuGlnLeuAlProleuSerSerleuAnthrValleuSerGlnAla 63
 DB 1119 ATGTTGGTATGAGATTAGCTCCAGAGGTTCTTGATGCGCTTCACAGACAAA 1178
 QY 64 ArgAspSerSerPheIleProleuGlnHisMetleuThrGlnIleAlaTyrglnIle 83
 DB 1179 GCACG-----CTCACTAGAACCTACAGACAGAGATTGCACTCCAGTA 1223
 QY 84 AlaSerGlyLeuAlaTyrlleuHisIleIleValSerIleIlePheCysAspLeuSerAsp 103
 DB 1224 GCTGATGTTGATGATCTCCACCTCCAGCCCATGATATATATCCAGAGCTGAAACCC 1283
 QY 104 AsnIleLeuValIlePheSerleuAspValIleGlnHisIleAsnIleIleSerAspTy 123
 DB 1284 AATGTGCGCTTTTCACTGATGCCAATGCCAATGCCAATGCCAATGCCAATGCCA 1343
 QY 124 GlyIleSerArgIleSerPheHisIleGlnValAlaleuGlnValGlnGlyThrProGly 143
 DB 1344 GGCATTGCTCACTGCTGTAGAAATGGGATTAATAACATCAGAGGACACACAGGCTT 1403
 QY 144 GlnAlaProGlnIle---ArgProArgIleValTyrlasGlnValIleAspMetPheSer 162
 DB 1404 CGTGCACCTGAAAGTTCAGAGAAATGCTATTTATACCAACAGGCTGATTTATCA 1463
 QY 163 TyrlGlyMetValleuTyrlGlnleuLeu---SerGlnIleArgProAlaIleuGly----- 179
 DB 1464 TTGGTTTACTACTGATGACATTTTGACAACTGAGGTAAATAGTAGAGGTTTGAA 1523
 QY 180 -----HisIleGlnleuGlnIleAlaIleValIleSerIleGlyIleArgPro 195
 DB 1524 TTTCAAATGAGTGTGATGATTAAGAAATACAGAAATTTCTGATCCAGTTAAAGAA 1583
 QY 196 ValIleuGlnProGlnGlnValGlnPheArgIleGlnAlaIleuMetMetGlnCys 215
 DB 1584 TATGTTGTGCCCA-----TGGCCTATGCTTGAAGAAATTAATAACAGTGT 1631
 QY 216 TrpAspThrIleProGlnIleArgProleuAlaIleuSerValIleSerGlnMetIleAsp 225
 DB 1632 TTGAAGAAATCCCAAGAAAGGCTTCTCTGCCAGGATTTCTCTCAGGCTTTGAC 1691
 QY 236 ProThrPheAlaThrPheMetTyrlGlnleuCysCysGlyIleGlnIleAlaPhe----- 253
 DB 1692 ATTTGAATTCAGCT-----GAATTAAGTGTCT- GACGAGAGAGCATTTATTAAC 1741
 QY 254 -----PheSerSerGlnGlnGlnGln-----Tyr 261
 DB 1742 TAAAAAGTAATGTTGAATGATGATGCTGCTACATACATACACAGCAGAAATGCAAGAT 1801
 QY 262 ThrValIlePheTrpAspGlyIleGlnIleSerArg-AsnTyrlThrValIleAsnThrG 281
 DB 1802 TTGGCTGGGCTGTGGCACAACGACAGAGAGAGCTCATTTCTTGACTTAATATGTA 1861
 QY 281 ulysGlyIleuMetGlnVal-----GlnArgMetCysCysProGlyMetIleValSe 298
 DB 1862 AGGATACACTTCTGAGGAAGTGTGATAGTAAATATGTTAGCTTACGCTTG----- 1913

QY 298 rCysGlnleuGlnValGlnArgSerleuTrp-----ThrAlaThrGlnAspGlnIle 316
 DB 1914 -GTGCATCTTCCTGTGAAAGAAAGAGCTGATGTTGCTGGACACAGTCTGTACTCT 1972
 QY 316 eTyrlleTyrlThrleuGlyIleCysProleuAnthrProGlnGlnAlaIleuAspThr 336
 DB 1973 CCGTGTCATCAATACCGAAGATGGGAAAAAGACATACCTCCAGAAAGATGACTGATTC 2032
 QY 336 rProAlaValIleThrCysPheleuAlaValProValIleIle-----IleAsnSerTy 354
 DB 2033 T-----GTCACTGTTGTTGATTGCAATTCCTTTTCAAGCAAGCAACAAAAA 2083
 QY 354 rIleuValleuAlaGlyLeuAlaAspGlyLeuValAlaValAlaPhe 368
 DB 2084 TTTTCTTTGTTGTAACCGCTGATGCAAGTTAGCAATTTT 2126

RESULT 9
 US-10-115-482-49
 / Sequence 49, Application US/10115482
 / Publication No. US20030212257A1
 / GENERAL INFORMATION:
 / APPLICANT: Syntex, et al.
 / TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM
 / TITLE OF INVENTION: AND METHODS
 / TITLE OF INVENTION: OF USING THE SAME
 / FILE REFERENCE: 21404-322D
 / CURRENT APPLICATION NUMBER: us/10/115,482
 / PRIOR FILING DATE: 2002-04-05
 / PRIOR APPLICATION NUMBER: 60/281,086
 / PRIOR FILING DATE: 2001-04-03
 / PRIOR APPLICATION NUMBER: 60/281,136
 / PRIOR FILING DATE: 2001-04-03
 / PRIOR APPLICATION NUMBER: 60/281,863
 / PRIOR FILING DATE: 2001-04-05
 / PRIOR APPLICATION NUMBER: 60/281,906
 / PRIOR FILING DATE: 2001-04-05
 / PRIOR APPLICATION NUMBER: 60/282,934
 / PRIOR FILING DATE: 2001-04-10
 / PRIOR APPLICATION NUMBER: 60/283,512
 / PRIOR FILING DATE: 2001-04-12
 / PRIOR APPLICATION NUMBER: 60/285,325
 / PRIOR FILING DATE: 2001-04-19
 / PRIOR APPLICATION NUMBER: 60/285,890
 / PRIOR FILING DATE: 2001-04-23
 / PRIOR APPLICATION NUMBER: 60/286,068
 / PRIOR FILING DATE: 2001-04-24
 / PRIOR APPLICATION NUMBER: 60/286,292
 / PRIOR FILING DATE: 2001-04-25
 / PRIOR APPLICATION NUMBER: 60/287,213
 / PRIOR FILING DATE: 2001-04-27
 / PRIOR APPLICATION NUMBER: 60/288,257
 / PRIOR FILING DATE: 2001-05-02
 / PRIOR APPLICATION NUMBER: 60/291,134
 / PRIOR FILING DATE: 2001-05-15
 / PRIOR APPLICATION NUMBER: 60/282,020
 / PRIOR FILING DATE: 2001-04-06
 / PRIOR APPLICATION NUMBER: 60/291,725
 / PRIOR FILING DATE: 2001-05-17
 / PRIOR APPLICATION NUMBER: 60/294,771
 / PRIOR FILING DATE: 2001-05-31
 / PRIOR APPLICATION NUMBER: 60/296,965
 / PRIOR FILING DATE: 2001-06-08
 / PRIOR APPLICATION NUMBER: 60/299,128
 / PRIOR FILING DATE: 2001-06-08
 / NUMBER OF SEQ ID NOS: 149
 / SEQ ID NO 49
 / LENGTH: 3040
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: (108)..(2841)
 / US-10-115-482-49


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QY 104 Aenlleleuvaltpserleuaspvalylsglnhisileasnlleuyserseraptyr 123
D 3886 AATGCTGCTTTTACACTGTATCCCATCTCCCATCTTCATTCGAAAGATGCTGCTAC 3945
QY 124 GYIleaserarglnserpheniglnlglvalaleuylvalgluglytprprogltyr 143
D 3946 GGCAATTCCTCAGTACTGCTGTAGAAATGGGATMAAAACATCAGAGGACACACAGGCTTT 4005
QY 144 Glnalaprogluile---Argproargilevaltyrpsgluysvalasmetpheneser 162
D 4006 CGTGACCTGAAGTTGGCCAGAGAAATGCTATTATACCAACAGCGCTGATTTATTC 4065
QY 163 Tyrglymevalleutyrgluileu---serglylnargproalaleugly----- 179
D 4066 TTGGTTTACTACTATGACATTTTGCAACGTAGAGTGAATAGTAGAGGGGTTGAAG 4125
QY 180 -----Hisiglnleuqlnlealealysleuserlysglyleargpro 195
D 4126 TTCCAAATGAGTTGATGATTAAGAAATACAGAGAAATTAACCTGATCCAGTTAAAGAA 4185
QY 196 Valleuylglnproglugluvalglnpheargyleuqlnaleuemetegluys 215
D 4186 TATGCTTGTGCCCCA-----TGCCCTATGTTGAGAAATTAATTAACAGTGT 4233
QY 216 Trraspthrlysprogulysargproleualaleuservalyalserglnmetlysasp 235
D 4234 TTGAAGAAATCCCTCAGAAAGGCTTCTGCCCCAGCTTTGCATTTGAATTC 4293
QY 236 Prothrphenialath-phenetyrgluileucyscysglyysglnthralaphe----- 253
D 4294 GCT-----GAAATGCTGTCT-GACGAGAGCATTTTATTACC 4331
QY 254 -----pheneserglnlyglnlyu-----Tyr 261
D 4332 TAAAAACGTAAATTGTTGATGCATGCTGCTACACATACACAGCGAAGTCAGACAT 4391
QY 262 Thrvalvalpheitraspdylysglnleuserarg-asnlythrvalvalenthrgl 281
D 4392 TTGGCTGGGCTGTGGGACACCCGACAGACAGAGCTCATTTTGTACTTAATACTGA 4451
QY 281 Ilysglyleuemetgluval-----Glnargmetcyscysproglymetylvalse 298
D 4452 AGGATACACTCTGTGAGAAATGCTGATAGTAATGATGCTTACCTTG----- 4503
QY 298 rcysglnleuqlnvalglnargserleutpr-----Thralathrglnspglnlyseil 316
D 4504 -GTGCATCTTCCGTGAAAGAAAGAGTGTGTGTCTGTGGACACAGCTGTACTCT 4562
QY 316 eTyrlleutythrleuylsglymetcysproleuasnthrproglnglnalaleuapth 336
D 4563 CCTGTCATCAATACCGAAGATGGAAAAAGACATACCTTAAGAAAGTACTGATTC 4622
QY 336 rProalavalvalthrcyspheleualavalprovalillelys-----lysasenserty 354
D 4623 T-----GTCACTTGTGTATGTGCAATTCCTTTCCAGAAAGCAAAACAAAAA 4673
QY 354 rleuvalleuvalaglyleualaspglyleuvalalavalphe 368
D 4674 TTTCTTTGTTGTTGAACCGCTGATGCAAGTTACCAATTTTT 4716

```

RESULT 11 US-10-335-687A-6

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; Sequence 6, Application US/10335687A
; Publication No. US2003016622A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 39267, Human Kinase Family Members and
; TITLE OF INVENTION: Uses Therefor
; FILE REFERENCE: MP102-001PRM
; CURRENT APPLICATION NUMBER: US/10/335,687A
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: 60/345,773

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; PRIOR FILING DATE: 2002-01-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 5475
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(5475)
; US-10-335-687A-6

Alignment Scores:
Pred. No.: 2,09e-25 Length: 5475
Score: 330.50 Matches: 108
Percent Similarity: 47.34% Conservative: 79
Best Local Similarity: 27.34% Mismatches: 150
Query Match: 8.65% Indels: 59
DB: 13 Gaps: 14

US-09-836-392-21 (1-728) x US-10-335-687A-6 (1-5475)

QY 10 Alawetlyshnpheneserglu-----Pheargglnlglalasermet 23
D 3601 GCTGTGAAGATTTTATTAATAAACAATACATCACTCAGGCTGTTAAGACAGAGCTTGCTG 3660
QY 24 Leuhsalaleuqlnhisprocytilevalaleuileglylleserilehsproleu 43
D 3661 CTTTGCACCTCCACACCCAGTTGATATCTTTGCTGGACAGTGGATTCCTCCCG 3720
QY 44 Cysphealaleuqlnleualaproleuserserleuasnthrvalleusergluasnala 63
D 3721 ATGTTGGATGAGATTAGCTCAGCTCCAGGTTCTTGATGCGCTCTCAGACGACAA 3780
QY 64 Argasrsererphelleproleuqlnhemleuthrglnlylalealyglnle 83
D 3781 GCCAGC-----CTCAGTACAACTTCACAGACAGATTCAGCTCCACGTA 3825
QY 84 Alasegryleualatyrlleuhslylyshnlelephecysaspleuysaspr 103
D 3826 GCTGATGTTTGAATACSTCCATCAGCATGATTAATAACGAGACCTGAACCCAC 3885
QY 104 Aenlleleuvaltpserleuaspvalylsglnhisileasnlleuyserseraptyr 123
D 3886 AATGCTGCTTTTACACTGTATCCCATCTCCCATCTTCATTCGAAAGATGCTGCTAC 3945
QY 124 GYIleaserarglnserpheniglnlglvalaleuylvalgluglytprprogltyr 143
D 3946 GGCAATTCCTCAGTACTGCTGTAGAAATGGGATMAAAACATCAGAGGACACACAGGCTTT 4005
QY 144 Glnalaprogluile---Argproargilevaltyrpsgluysvalasmetpheneser 162
D 4006 CGTGACCTGAAGTTGGCCAGAGAAATGCTATTATACCAACAGCGCTGATTTATTC 4065
QY 163 Tyrglymevalleutyrgluileu---serglylnargproalaleugly----- 179
D 4066 TTGGTTTACTACTATGACATTTTGCAACGTAGAGTGAATAGTAGAGGGGTTGAAG 4125
QY 180 -----Hisiglnleuqlnlealealysleuserlysglyleargpro 195
D 4126 TTCCAAATGAGTTGATGATTAAGAAATACAGAGAAATTAACCTGATCCAGTTAAAGAA 4185
QY 196 Valleuylglnproglugluvalglnpheargyleuqlnaleuemetegluys 215
D 4186 TATGCTTGTGCCCCA-----TGCCCTATGTTGAGAAATTAATTAACAGTGT 4233
QY 216 Trraspthrlysprogulysargproleualaleuservalyalserglnmetlysasp 235
D 4234 TTGAAGAAATCCCTCAGAAAGGCTTCTGCCCCAGCTTTGCATTTGAATTC 4293
QY 236 Prothrphenialathphenetyrgluileucyscysglyysglnthralaphe----- 253
D 4294 GCT-----GAAATGCTGTCT-GACGAGAGCATTTTATTACC 4331

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QY 254 -----PheSerSerGlnGlnGlu-----Tyr 261
Db 4332 TAAAGAGTAATGTTGAATGATGCTGTCACATCACACAGGAGATGCAAGCAT 4391
QY 262 ThrValValPheTyrAspGlyLysGlnGluSerArg-AsnTyrThrValValAsnThrG1 281
Db 4392 TTGGCTGGGCTGTGGGACACACGACAGACAGCTGCTCATTTCTTGAATTAATCTGA 4451
QY 281 uLysGlyLeuMetGluVal-----GlnArgMetCysCysProGlyMetLysValSe 298
Db 4452 AGGATACACTTCTGAGGAAGTGTGATAGTAGATATGTGCTTACCTTG----- 4503
QY 298 rCysGlnLeuGlnValGlnArgSerLeuTyr-----ThrAlaThrGlnAspGlnLysS11 316
Db 4504 -GTGATCTTCTCTGTGAAAAGAAAGTGTGCTGTGTCGGACACAGTGTGCTACTCT 4562
QY 316 eTyrIleTyrThrLeuLysGlyMetCysProLeuAsnThrProGlnGlnAlaLeuSph 336
Db 4563 CCGTGTCAATCAATACCGAAGATGGGAAAAGACATACCTAGAAAAGATGACTGATTC 4622
QY 336 rProAlaValAlaThrCysPheLeuAlaValProValIleLys-----LysAsnSerTy 354
Db 4623 T-----GTCACTGTGTGTATGCAATTCCTTTCCAAAGCAACCAACAAAAA 4673
QY 354 rLeuValLeuAlaGlyLeuAlaAspGlyLeuValAlaValPhe 368
Db 4674 TTTCTTTTGTGTGGAACCGCTGATGCAAGTGTGCAATTTT 4716

RESULT 12
US-10-335-687A-1
/ Sequence 1, Application US/10335687A
/ Publication No. US20030166222A1
/ GENERAL INFORMATION:
/ APPLICANT: Meyers, Rachel E.
/ TITLE OF INVENTION: Millennium Pharmaceuticals, Inc.
/ TITLE OF INVENTION: 39267, Human Kinase Family Members and
/ FILE REFERENCE: MP102-001PRNM
/ CURRENT APPLICATION NUMBER: US/10/335,687A
/ PRIOR FILING DATE: 2003-01-02
/ PRIOR APPLICATION NUMBER: 60/345,773
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 5799
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ NAME/KEY: CDS
/ LOCATION: (29)...(5485)
US-10-335-687A-1

Alignment Scores:
Pred. No.: 2,29e-25 Length: 5799
Score: 330.50 Matches: 108
Percent Similarity: 47.34% Conservative: 79
Best Local Similarity: 27.34% Mismatches: 150
Query Match: 8.65% Indels: 59
DB: 13 Gaps: 14

US-09-836-392-21 (1-728) x US-10-335-687A-1 (1-5799)
QY 10 AlaMetLysAsnPheSerGlu-----PheArgGlnGlnAlaSerMet 23
Db 3629 GCTGTGAAGATTTTAAATAAACATACACTCAGCGCTGTAAACAGAGCTTGTGTG 3688
QY 24 LeuHisAlaLeuGlnHisProCysIleValAlaLeuIleGlyIleSerIleHisProLeu 43
Db 3689 CTTTGCCACCTCCACACACCCAGTTTGTATCTTGTGCGAGCTGGAGATTCTCCCGG 3748
QY 44 CysPheAlaLeuGlnLeuAlaProLeuSerSerLeuAsnThrValLeuSerGluAsnAla 63

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Db 3749 ATGTGTGATGAGGTAGCTCCAAAGGTTCTCTTGATCGCTGCTTACAGCAGCAAA 3808
QY 64 ArgAspSerSerPheIleProLeuGlnLysMetLeuThrGlnLysIleAlaTyrGlnIle 83
Db 3809 GCCAGC-----CTCACAGAAACCTTCACGACACAGATTGACATCCACAGTA 3853
QY 84 AlaSerGlyLeuAlaIleTyrLeuHisLysLysAsnIleIlePheCysAspLeuLysSerAsp 103
Db 3854 GCTAGAGTTTGAGATACCTCCACTCAGCCATGATATATACGAGACCTGAAACCCCA 3913
QY 104 AsnIleLeuValTyrSerLeuAspValLysGlnHisIleAsnIleLysLeuSerAspTyr 123
Db 3914 AATGTGCTGCTTTACACACTGTATCCCAAGCTGCCATCTTGCAGAAAGTTGTGACTTC 3973
QY 124 GlyIleSerArgIleSerPheHisGlyValAlaLeuGlyValGluGlyThrProGlyTyr 143
Db 3974 GGCATGTCTCACTGCTGTAGAAATGGGATTAACATCAAGAGGACACACAGGGTTT 4033
QY 144 GlnAlaProGluIle---ArgProArgIleValTyrAspGlnLysValAspMetPheSer 162
Db 4034 CGTGCACTGAAGTGCACAGAGAAATGTCTATTATACCAAGGCTGATGTATTTC 4093
QY 163 TyrGlyMetValLeuTyrGluLeuLeu---SerGlyGlnArgProAlaLeuGly----- 179
Db 4094 TTTGGTTTACTACTCTATGACATTTTGACAACTGGAGGTAGATAGAGGTTTGAAG 4153
QY 180 -----HisHisGlnLeuGlnIleAlaLysLysLeuSerLysGlyIleArgPro 195
Db 4154 TTTCCAAATGATGTTGATGATTAAGAAATACAGAAATATACCTGATCCAGTTAAAGAA 4213
QY 196 ValLeuGlyGlnProGluGlnValGlnPheArgArgLeuGlnAlaLeuMetMetGlyCys 215
Db 4214 TATGTTGTGCCCA-----TGCCATAGTTGAGAAATTAATTAACAGTGT 4261
QY 216 TrpAspThrLysProGluLysArgProLeuAlaLeuSerValValSerGlnMetLysAsp 235
Db 4262 TTGAAGAAATACCTCAAGAAAGCCATCTTCCGACAGTCTTTGACATTTGAAATGA 4321
QY 236 ProThrPheAlaThrPheMetTyrGluLeuCysCysGlyLysGlnThrAlaPhe----- 253
Db 4322 GCT-----GATTAAGTGTGCT--GACAGACGCAATTTATATAC 4359
QY 254 -----PheSerSerGlnGlnGlu-----Tyr 261
Db 4360 TAAAGAGTAATGTTGAATGATGATGCTGCTACACATCACACAGCAAGATGCAAGCAT 4419
QY 262 ThrValValPheTyrAspGlyLysGlnGluSerArg-AsnTyrThrValValAsnThrG1 281
Db 4420 TTGGCTGGGCTGTGGGACACACGACAGACAGCTCTCATTTCTTGAATTAATCTGA 4479
QY 281 uLysGlyLeuMetGluVal-----GlnArgMetCysCysProGlyMetLysValSe 298
Db 4480 AGGATACACTTCTGAGGAAGTGTGATAGTAGATATGTGCTTACCTTG----- 4531
QY 298 rCysGlnLeuGlnValGlnArgSerLeuTyr-----ThrAlaThrGlnAspGlnLysS11 316
Db 4532 -GTGATCTTCTCTGTGAAAAGAAAGTGTGCTGTGTCGGACACAGTGTGCTACTCT 4590
QY 316 eTyrIleTyrThrLeuLysGlyMetCysProLeuAsnThrProGlnGlnAlaLeuSph 336
Db 4591 CCGTGTCAATCAATACCGAAGATGGGAAAAGACATACCTAGAAAAGATGACTGATTC 4650
QY 336 rProAlaValAlaThrCysPheLeuAlaValProValIleLys-----LysAsnSerTy 354
Db 4651 T-----GTCACTGTGTGTATGCAATTCCTTTCCAAAGCAACCAACAAAAA 4701
QY 354 rLeuValLeuAlaGlyLeuAlaAspGlyLeuValAlaValPhe 368
Db 4702 TTTCTTTTGTGTGGAACCGCTGATGCAAGTGTGCAATTTT 4744

RESULT 13
US-10-335-687A-4

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/ Sequence 4, Application US/10335687A
/ Publication No. US20030166222A1
/ GENERAL INFORMATION:
/ APPLICANT: Meyers, Rachel E.
/ TITLE OF INVENTION: Millennium Pharmaceuticals, Inc.
/ TITLE OF INVENTION: 39267 Human Kinase Family Members and
/ TITLE OF INVENTION: Uses Therefor
/ FILE REFERENCE: MP102-001P1RUM
/ CURRENT APPLICATION NUMBER: US/10/335,687A
/ CURRENT FILING DATE: 2003-01-02
/ PRIOR APPLICATION NUMBER: 60/345,773
/ PRIOR FILING DATE: 2002-01-02
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 5817
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (29)...(5503)
/ US-10-335-687A-4

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Alignment Scores:
Pred. No.: 2,3e-25 Length: 5817
Score: 330.50 Matches: 108
Percent Similarity: 47.34% Conservative: 79
Best Local Similarity: 27.34% Mismatches: 150
Query Match: 8.65% Indels: 59
Gaps: 14
US-09-836-392-21 (1-728) x US-10-335-687A-4 (1-5817)

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QY 10 AlaMetIyAsnPhSerGlu-----PheArgInGluAlaSerMet 23
DB 3629 GCGTGAAGATTATTAATACATACATCACTCAAGCTGTAAACAGAGCTTGCGTG 3688
QY 24 LeuHsAlaLeuGlnHsIspProCysIleValAlaLeuIleGlyIleSerIleHsProLeu 43
DB 3689 CTTGGCACCTCCACACACCCAGTTGATCTTGTGCGAGCTGGAGATTCCGCCCGG 3748
QY 44 CysPheAlaLeuGlnAlaProLeuSerSerIleuAntRValLeuSerGluAla 63
DB 3749 ATGTGGTGAAGATTAGCTCCACAGGCTTCCTTGATCCCGCTTCACAGAGAA 3808
QY 64 ArgAspSerSerPheIleProLeuGlyHsMetLeuThrGlnIleValIleAlaTy 83
DB 3809 GCCAGC-----CTCACTGAACCTTACAGCAGAGATTGCATCCAGCTA 3853
QY 84 AlaSerGlyLeuAlaTyIleuHsIleuValAsnIleIlePheCysAspLeuIleSer 103
DB 3854 GCTGATGCTTGAATACCTCCACAGCTCATGATTAATATCCAGAGCTGAACCCAC 3913
QY 104 AsnIleLeuValIlePheSerIleuAspValIleGlnHsIleuValIleuSerAsp 123
DB 3914 AATGCTGCTCTTTCACACTGATATCCCAATGCTGCATCATTCGAAAGATTGCTG 3973
QY 124 GlyIleSerArgIleSerPheHsIleuGlyAlaLeuGlyValIleGlyIlePro 143
DB 3974 GGCATTGCTCACTACTGCTGTAGATGGGATTAATAACATCAGAGGCGACCCAG 4033
QY 144 GlnAlaProGluIle---ArgProArgIleValIlePheGlnIleValIleuSer 162
DB 4034 CGTGACCTGAAGTTGCCAGAGAAATGCTATTATTAACCAAGGCTGATTTATCA 4093
QY 163 TyrGlyMetValIleuTyIleuLeu---SerGlyGlnArgProAlaLeuGly----- 179
DB 4094 TTGGTTTACTACTCATGACATTTTGACAACTGAGAGTAGAATAGTAGAGGTTGAG 4153
QY 180 -----HisIleGlnIleuGlnIleAlaIleValIleuSerIleuValIleArgPro 195
DB 4154 TTTCAAATAGAGTTGATTAATTAAGAAATTAAGAAATTAAGAAATTAAGAA 4213

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QY 196 ValLeuGlyIleProGlnIleValIleGlnPheArgIleuGlnAlaLeuMetCys 215
DB 4214 TATGTTGTGCCCA-----TGCCCTATGTTGAGAAATTAATTAACAGCTGT 4261
QY 216 TrpAspThrIleuProGlnIleuValIleuSerValIleuSerGlnIleuVal 235
DB 4262 TTGAAGAAATCTCAAGAAAGCTTACTTGCCTCCAGCTCTTTACATTTGAATTCA 4321
QY 236 ProThrPheAlaThrPheMetTyIleuLeuCysGlyIleValIleuAlaPhe----- 253
DB 4322 GCT-----GAATTAGTGTGCT- GACAGAGCATTTTATTACC 4359
QY 254 -----PheSerSerGlnIleGlnIle-----Tyr 261
DB 4360 TAAAGCTAATTGTTGAATGATGCTGTGATCAATCAACACAGAGGAAATGCAAGCAT 4419
QY 262 ThrValIlePheThrPheArgIleuGlnIleuSerArg-AsnTyIleThrValIle 281
DB 4420 TTGGCTGAGCTGTGGGACACAGCAGAGAGAGCTCTCATTTCTTGACTTAATCTGA 4479
QY 281 uIleGlyIleuMetCysIleVal-----GlnArgMetCysCysProGlyMetIleVal 298
DB 4480 AGGATACACTTCTGAGAGAGCTGTGATGATGATGATGATGATGATGATGATGATG 4531
QY 298 rCysGlnIleuGlnIleValIleuSerIleuThrPhe-----ThrAlaThrGlnAsp 316
DB 4532 -CTGCATCTTCTGCTTAAAGAAAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 4590
QY 316 eTyIleTyThrIleuValIleuSerIleuValIleuSerIleuValIleuSer 336
DB 4591 CCTGCTGATCAATCAACAGATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4650
QY 336 rProAlaValIleThrCysPheLeuAlaValIleValIleValIleValIleVal 354
DB 4651 T-----CTCACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 4701
QY 354 rLeuValLeuAlaGlyLeuAlaAspGlyLeuValAlaValIlePhe 368
DB 4702 TTTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 4744

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RESULT 14

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US-09-836-347-226
/ Sequence 226, Application US/09969347
/ Patent No. US20020115085A1
/ GENERAL INFORMATION:
/ APPLICANT: Ebner, Reinhard
/ TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
/ TITLE OF INVENTION: Sets
/ FILE REFERENCE: 689295-68
/ CURRENT APPLICATION NUMBER: US/09/969,347
/ CURRENT FILING DATE: 2001-10-02
/ PRIOR APPLICATION NUMBER: US/60/237,598
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: US/60/237,604
/ PRIOR FILING DATE: 2000-10-03
/ NUMBER OF SEQ ID NOS: 318
/ SOFTWARE: Patent In version 3.0
/ SEQ ID NO 226
/ LENGTH: 3454
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-969-347-226

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Alignment Scores:
Pred. No.: 3.68e-23 Length: 3454
Score: 307.50 Matches: 178
Percent Similarity: 35.43% Conservative: 87
Best Local Similarity: 23.80% Mismatches: 272
Query Match: 8.05% Indels: 212
Gaps: 31
DB: 10

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US-09-836-392-21 (1-728) x US-09-969-347-226 (1-3454)

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19 GlnGluAlaSerMetLeuHisAlaLeuGlnHisProCysIleValAlaLeuIleGlyLe 38
718 CAGAAAGCCCGCTCTTTGGAGCCCTTCAGACACCCCAACAATAATGGCCCTTAGGGGGCC 777
39 SerIleHisPro-----LeuCysPheAlaLeuGluLeuAlaProLeuSerSerLeuAsn 56
778 TGCCCTCAACCCCAACACCTCTGCTAGTATGAGATGCGCGGGGTGTGACTGAGC 837
57 ThrValLeuSerGluAsnAlaArgAspSerPheIleProLeuGlyHisMetLeuThr 76
838 AGGGTGTCTGGCAGGTGCGCGG-----GTGCCA---CCTCAGCTGTGGTC 879
77 GlnLysIleAlaTyrGlnIleAlaSerGlyLeuAlaTyrLeuHisLysLys----- 93
880 ---AACTGGGCTGTGAGTGGCGCGGGGATGACTACCTACCAATGATGCCCTGTG 936
94 AsnIleIlePheCysAspLeuLysSerAspAsnIleLeuValTrpSerLeuAspValLys 113
937 CCTCATCTCCACCGGAGCTCAAGTCCATCACTCTGATC-----CTGGAGGCCATC 990
114 GluHisIleAsn-----IleLysLeuSerAspTyrGlyIleSerArgGln 128
991 GAGAACCAACACCTCGCAGACAGGTGTCAAGATCACGGACTTCGGCCCTCGCCCGCAG 1050
129 SerPheHisGluGlyAlaLeuGlyValGluGlyThrProGlyTyrGlnAlaProGluIle 148
1051 TGGCAACAAGACCACCAAGATGAGCGCTCGCGGACCTACCGCTGGATGGCGCGAGGT 1110
149 ArgProArgIleValTyrAspGluLysValAspMetPheSerTyrGlyMetValLeuTyr 168
1111 ATCCGTCTCTCCCTCTCTCCAAAGCAGTATGATCTGGAGCTTCGGGGTGTCTGTGTG 1170
169 GluLeuLeuSerGlyGlnArgProAlaLeuGlyHisIleGlnLeuGlnIleAla----- 186
1171 GAGCTGTGACGGGGAGGTCCCTACCGTGAATCGACCCCTTGACCGTGGCGTATGGC 1230
187 -----LysLysLeuSerLysGlyIleArgProValLeuGlyGlnProGluGluVal 203
1231 GTGGCTATGAATAAGCTGACCTGCCATTCCTCCACGTGCCCGCGAGCC----- 1281
204 GlnPheArgArgLeuGlnAlaLeuMetMetGlyCysTrpAspThrLysProGluLysArg 223
1282 ---TTTGCCCGC-----CTCTCGAGAAATGCTGGGACCCAGACCCCAACCGGGCGG 1329
224 ProLeuAlaLeuSerValValSerGlnMetLysAspProThrPheAlaThrPheMetTyr 243
1330 -----CCAGATTCTGTAGCATCTTGAG 1353
244 GluLeuCysCysGlyLysGlnThrAlaPhePheSerSerGlnGlyGlnTyrThrVal 263
1354 CGCTTGAAATCATGCAACAGTCAAGCCCTGTTCCAGATGCCACTGGAGTCTTCCACTCG 1413
264 ValPheTrpAspGlyLysGluGluSerArgAsnTyr-----ThrValAlaAsnThrGlu 281
1414 CTGCAGGAAGACTGGAAGCTGAGATTACACATGTTTATGATACCTTCGACCAAGAGAG 1473
282 LysGlyLeuMetGlu-ValGlnArgMetCysCys-----ProGlyLe 295
1474 AAGGAGCTTCGGAGCCGTGAGAGAGAGTCTCGCGGGCGCACAGAGCAGCGCTTCCAG 1533
295 tLysValSerCys-----GlnLeuGlnValGlnArgSerLeuThrAlaThrGln 312
1534 GAGAGAGCTTCGGCGGGGGGAGCAGGAGCTCGCGGGCGCACAGAGCAGCGCTTCCAG 1585
312 uAspGlnLysIleTyrThrLeuLysGlyMetCysProLeuAsnThrProGlnGln 332
1586 -----TCGTGGAACGGGAGCTGCACCTGCTCATGTGCCAGCTG 1623
332 nAlaLeuAspThrPro----- 337
1624 AGCCAGGAGAAGCCCGGGTCCGCAAGCGCAAGGCAACTTCAAGCGCAGCGCCTGTCT 1683
338 -----AlaValValThrCysPheLeuAlaValProValIleLysLys 351

1684 AAGCTGCGGGAAGCGCGCAGCATCAGCTGCTGCTCTGCTTTGAGCATAGATCACA 1743
351 sAsnSerTyrIleuValLeuAlaGlyLeuAlaAspGlyLeuValAlaValPhePro----- 369
1744 GTCCAGGCTCTCCAACTCTG-GATAAGCGGAAGGATCCGATGGGGGCCAGCCCCCTGC 1802
370 -----ValValArgGlyThrProLysAspSerCys 380
1803 AAGCCCGAGCATATCCCCCGCTGAGGGCCATTGCTGACTCCCGTGGAC----- 1854
380 rTyrLeuCysSerHisThrAlaAsnArgSerLysPheSerIleAlaAspGluAspAlaAr 400
1855 -----TGTGGTGGCAGCAGCATGTCACGACGAGTGGAGGAAGTGGGACATGGAGCGG 1907
400 sGlnAsnProTyrProValLys----- 407
1908 CGTGGGGCC-----CCAAAGAGGAGAGTGTGCGGGGCAAGAAGGAGGACGACGTG 1964
408 -----AlaMetGluValVa 412
1965 GGGCCCGCAGCTCCACCTGCGAAGGAGCGGTGGGAGGAGGAGGAGGCTGAAGGGCT 2024
412 lAsnSerGlySerGluValTrpTyrSerAsnGlyProGlyLeu----- 426
2025 GGGGAAGGAGGAACACAGTGTCAATGTCGCCCAACCTGGGCAAGTCCCCCAACA 2084
427 -----LeuValIleAspCysAlaSerLeuGluIleCysArgArgLeu----- 440
2085 CACACCATCGCCCTGGCTTCGCCAGCTCAATGATGAGAGGAGTTCGCGGAGGCAGA 2144
441 -----GluProTyrMetAlaProSerMetValThrSerVa 452
2145 GGATGGAGGAGCAGCGTGCCTTCCTCCCTTCTACGACCCGCTCTACCTCTCAGTGC 2204
452 lValCysSerSerGluGlyArgGlyGluGluValTrpCysLeuAspAspLysAlaAs 472
2205 ACTGCTCGCGAGCCCTCCCGGGGCGCGGGCGCGTGGAGCGCAGCGCTTCGCGCC 2264
472 nSerLeuValMetTyrHisSerThrThrTyrGlnLeu-----CysAl 486
2265 CCGCGCTCGGTGGGACACGCGCGCGCGCGCTGCGACCTGGCGCTGCTAGGTGGCG 2324
486 a----- 486
2325 CAGCTGCTGGGGCTGTGGGCTGGGCGCGCAGCTGGCGGAGCGCGCGCGCGCAGCG 2384
487 -----ArgTyrPheCysGlyValProSerProLeuArgAspMetPheProVa 502
2385 TGAGGAGCAGCGCGCTGCTCGACGCGCTCTTCTTCCCGCGCGCGCGCTTCCCG-- 2442
502 lArgProLeuAspThrGluProProAlaAlaSerHisThrAlaAsnProLysValProGl 522
2443 -CGGGCGCTC-----AGCCCAACCGCGCTGCCCGCGCGCGCGCGCGCGCGCGCC 2495
522 uGlyAspSerIleAlaAspValSerIleMetTyrSerGluGluLeuGlyThrGlnIleLe 542
2496 CGGCTGGGCTGGCGCC-----TCGGCCACCT 2525
542 uIleHisGlnGluSerLeuThrAspTyrCysSerMetSerSerTyrSerSerSerProPr 562
2526 CGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2585
562 oArgGlnAlaAla-----ArgSerProSerSerLeuProSerProAlaSerSerSe 581
2586 TGACGAGCGCGCAGCGCGCGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2645
581 rValProPheSerThr-----AspCysGluAspSerAspMetLeuHisThrPr 597
2646 GCCTCGCGCAGCAGCAACCCCTGCTGAGCTGAGAGCTTCAAGAGGAGGAGCC 2705
597 oGly-----AlaAlaSerAspArgSerGluHi 606

2706 CGGCAGTGTCTACGCCGCCACCCACGTCACGGCTGTATGCGCTGTGTAGCCGCGGG---CA 2762

606

sAspLeuThrProMetAspGly 613

|||||
2763 CCGGCGGACGCCATCGGATGGG 2784

LT 15

0-171-581-312

quence 312, Application US/10171581

blication No. US20030104426A1

NERAL INFORMATION:

PLICANT: Dai, Hongyue

PLICANT: Linsley, Peter

PLICANT: Mao Mao

FILE OF INVENTION: Signature Genes in Chronic Myelogenous Leukemia

FILE REFERENCE: 9301-157-999

URRENT APPLICATION NUMBER: US/10/171,581

URRENT FILING DATE: 2002-06-14

RIOR APPLICATION NUMBER: 60/298,914

RIOR FILING DATE: 2001-06-18

UMBER OF SEQ ID NOS: 366

Q ID NO 312

LENGTH: 3454

TYPE: DNA

ORGANISM: Homo sapiens

URLICATION INFORMATION:

DATABASE ACCESSION NUMBER: X90846

DATABASE ENTRY DATE: 2001-06-18

0-171-581-312

ment Scores:

. No.: 3,688-23 Length: 3454

e.: 307.50 Matches: 178

ent Similarity: 35.43% Conservative: 87

y Local Similarity: 23.80% Mismatches: 272

Indels: 8.05% Indels: 212

Gaps: 15 Gaps: 31

9-836-392-21 (1-728) x US-10-171-581-312 (1-3454)

19 GlnGluAlaSerMetLeuHisAlaLeuGlnHisProCysIleValAlaLeuIleGlyIle 38

|||||
718 CAGGAAGCGCGCTTTGGAGCCCTCTGGAGCCCTCGAGCACCCCAACATAATTGCCCTTAGGGCGCC 777

39 SerIleHisPro-----LeuCysPheAlaLeuGluLeuAlaProLeuSerSerLeuAsn 56

|||||
778 TGCCTCAACCCCAACACCTCTGCTAGTGTAGTGTATGCCCGGGTGTGCTGACTGAGC 837

57 ThrValLeuSerGluAsnAlaArgAspSerPheIleProLeuGlyHisMetLeuThr 76

|||||
838 AGGGTGTCTGGCAGGTGCGCGG-----GTGCCA---CCTCAGTGTCTGGTC 879

77 GlnLysIleAlaTyrGlnIleAlaSerGlyLeuAlaTyrLeuHisLysLys----- 93

880 ----AACTGGCTGTCCAGTGGCCCGGCGCATGACTACCTACCAATGATGCCCTGTG 936

94 AsnIleIlePheCysAspLeuLysSerAspIleLeuValTrpSerLeuAspValLys 113

|||||
937 CCCATCATCCACCGGACCTCAAGTCCATCAACATCCTGATC-----CTGGAGGCCATC 990

114 GluHisIleAsn-----IleLysLeuSerAspTyrGlyIleSerArgGln 128

|||||
991 GAGAACCCACCACTCGCAGACAGGTGCTCAAGATCACGACTTCGGCCCTCGCCCGGAG 1050

129 SerPheHisGluGlyAlaLeuGlyValGluGlyThrProGlyTyrGlnAlaProGluIle 148

|||||
1051 TGGCAACAGACCAACCAAGATGAGCGCTCGGGGACCTAGCGCTGATGGCGCGGAGTT 1110

149 ArgProArgIleValTyrAspGluLysValAspMetPheSerTyrGlyMetValLeuTyr 168

|||||
1111 ATCCGCTCTCCCTCTCTCCAAAGCAGTGTCTGGAGCTTCGGGGTGTGCTGTGC 1170

169 GluLeuLeuSerGlyGlnArgProAlaLeuGlyHisGlnLeuGlnIleAla----- 186

1171 GAGTGTGTGACGGCGGAGGTCCTCCCTACCGTGAGATCGACGCTTGGCGCTGGCGTATGCG 1230

187 -----LysLysLeuSerLysGlyIleArgProValLeuGlnProGluGluVal 203

1231 GTGCTATGATTAAGCTGAGCTGCCCTTCCCTCCACGTCGCCCGAGCCC----- 1281

204 GlnPheArgArgLeuGlnAlaLeuMetMetGluCysTrpAspThrLysProGluLysArg 223

1282 ---TTTCCCGC-----CTCCTGGAGGAATGTGGGACCCAGACCCACCGGGGG 1329

224 ProLeuAlaLeuSerValSerGlnMetLysAspProThrPheAlaThrPheMetTyr 243

1330 -----CCAGATTTCGTAGCATCTTGAG 1353

244 GluLeuCysCysGlyLysGlnThrAlaPhePheSerSerGlnGlyGlnGluTyrThrVal 263

1354 CGGCTTGAAGTATCGAACAGTACGCTTCCAGATGCCACTGGAGTCCCTTCCACTCG 1413

264 ValPheTrpAspGlyLysGluGluSerArgAsnTyr-----ThrValValAsnThrGlu 281

1414 CTGAGGAAGACTGGAGCTGAGATTCAGACATGTTTGTGATGACCTTCGGACCAAGGAG 1473

282 LysGlyLeuMetGlu-ValGlnArgMetCysCys-----ProGlyLe 295

1474 AAGAGCTTCGGAGCCGTGAGGAGGAGCTGCTGGGGCGGCACAGGAGCAGCGCTTCCAG 1533

295 tLysValSerCys-----GlnLeuGlnValGlnArgSerLeuTrpThrAlaThrGlu 312

1534 GAGGACAGCTGCGCGCGGAGCAGGAGCTGGCAGAACGTGAGATGGACA----- 1585

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1586 -----TCGTGGAAACGGAGCTGCACCTGCTCATGTGCCAGCTG 1623

332 nAlaLeuAspThrPro----- 337

1624 AGCCAGGAGAAAGCCCGGGTCCCAAGCGCAAGGCACTTCAAGCGCAGCGCGCTGTCTC 1683

338 -----AlaValValThrCysPheLeuAlaValProValIleLysIle 351

1684 AAGTGGGGAAGCGCGCAGCCACATCAGCCTGCCCTTGGCTTTGAGCATAGATCACA 1743

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1744 GTCCAGCGCTCTCCAACTCTG-GATAAGCGGAAAGATCCGATGGGGCCAGCCCGCTGC 1802

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1803 AAGCCCGAGCATATCCCGCGCTGAGGCCATTCGCTGACTCCCGTGGAC----- 1854

380 rTyrLeuCysSerHisThrAlaAsnArgSerLysPheSerIleAlaAspGluAspAlaAr 400

1855 -----TGTTGGTGAGCAGCAGTGGCAGCAGTGGAGGAAGTGGGACATGGAGCGG 1907

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408 -----AlaMetGluValVa 412

1965 GGGGCCCGAGTCCACCTTCAGAGAGGCGGGTGGGAGGAGGAGGAGGCTGAGGGGCT 2024

412 lAsnSerGlySerGluValTrpTyrSerAsnGlyProGlyLeu----- 426

2025 GGGGGAAGGAAGCAACAGTGTGTATCAAGTCCCGCCCAACCTTGGGCAAGTCCCCCAACA 2084

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441 -----GluProTyrMetalProSerMetValThrSerVa 452

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486 a----- 486
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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on: December 14, 2003, 04:49:15 ; Search time 30.5 Seconds
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	295.5	7.3	859	1	US-08-395-580-2	Sequence 2, Appli
3	295.5	7.3	859	5	PCT-US95-02792-2	Sequence 2, Appli
4	279.5	6.9	394	4	US-09-345-473E-19	Sequence 19, Appli
5	268	6.6	663	4	US-09-252-991A-30843	Sequence 30843, A
6	267	6.6	668	1	US-08-205-018-2	Sequence 2, Appli
7	266	6.5	885	4	US-09-252-991A-26129	Sequence 16, Appli
8	261	6.4	1050	4	US-09-428-711A-16	Sequence 16, Appli
9	260	6.4	1093	4	US-09-252-991A-21827	Sequence 21827, A
10	259	6.4	1706	4	US-09-252-991A-31760	Sequence 31760, A
11	255.5	6.3	626	4	US-09-345-473E-43	Sequence 43, Appli
12	253	6.2	681	4	US-09-252-991A-24567	Sequence 24567, A

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Sequence 21, Appli	1037	4	US-09-428-711A-21
Sequence 36, Appli	2185	4	US-09-854-856-36
Sequence 4, Appli	2245	4	US-09-854-856-4

ALIGNMENTS

RESULT 1
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; Sequence 30843, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30843
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30843

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Percent Similarity:	31.29%	Conservative:	55
Best Local Similarity:	24.54%	Mismatches:	255
Query Match:	7.43%	Indels:	305
DB:	4	Gaps:	51
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 1982 TAAAGCCGAGAGCTGACTCCGATGGGGTCTGGTGGATGCTCCGCTGGTGGCAAGG 2041
 603 AlaProProArgProAlaArgArgValArgTrp-----ProTrp-----Arg 617
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 618 SerAlaArgCysSerProArgArgProThrProArgSerAla-----ProGlyAlaAla 635
 2102 GTGGGGCCCGAGGAGTTCGACATTTCTACCACTCTCTAGGAG 2146
 636 ThrGlyAlaPro-----ThrThrGlyAlaAlaArgProA-garg 648

18-395-580-2
 Sequence 2, Application US/08395580
 Patent No. 5676945
 GENERAL INFORMATION:
 APPLICANT: Ueharani R. Reddy, David Pleasure and the Children's
 Hospital of Philadelphia
 TITLE OF INVENTION: No. 5676945el Protein Kinase, Nucleic Acid
 NUMBER OF INVENTION: Sequences Encoding the Same and Methods Related Thereto
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5676945ris
 STREET: One Liberty Place - 46th Floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: U.S.A.
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIA TYPE: 3.5 inch disk, 720 Kb
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/395,580
 FILING DATE: herewith
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/205,018
 FILING DATE: 01-MAR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Rebecca L. Ralph (formerly Gaumond)
 REGISTRATION NUMBER: 35,152
 REFERENCE/DOCKET NUMBER: CH-0498
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-568-3100
 TELEFAX: 215-568-3439
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 859 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 08-395-580-2

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 : Local Similarity: 22.40% Mismatches: 257
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170 HisProAsnIleIleThrPheLysGlyValCysThrGlnAlaProCysfyrCysIleLeu 189
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; GENERAL INFORMATION:
; APPLICANT: Usharani R. Reddy, David Pleasure and the Children's
; APPLICANT: Hospital of Philadelphia
; TITLE OF INVENTION: Novel Protein Kinase, Nucleic Acid
; TITLE OF INVENTION: Sequences Encoding the Same and Methods Related Thereto
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Woodcock Washburn Kurtz Mackiewicz and Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02792
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/205,018
; FILING DATE: 01-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rebecca L. Ralph (formerly Gaumond)
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: CH-0488
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 859 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-02792-2

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Pred. No.: 2,148-14 Length: 859
Score: 295.50 Matches: 168
Percent Similarity: 34.2% Conservative: 89
Best Local Similarity: 22.4% Mismatches: 257
Query Match: 7.28% Indels: 236
DB: 5 Gaps: 31

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   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
496 GTGCTCTACAGTCTCTGCTCAGGAGCGCCCT----- 528
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
299 ValLeuTrpGluLeuLeuThrGlyGluIleProTyrLysAspValAspSerSerAlaIle 318
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
529 -----GCATCGGGCCACACAGCTCCAGATGTCAGAGAGCTGCCAAGGGCATCCGC 582
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
319 IleTrpGlyValGlySerAsnSerLeuHisLeu----- 329
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
583 CGGTTCCTGGGCGAGCGGAGAGTGCAGTTCGGGCGAGCTGCAGGCGCTCATGATGGAG 642
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
330 ProValProSerSerCysProAsp-----GlyPheLysIleLeuLeuLeuArgGln 345
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
643 TGTGGGACACTAAGCCAGAGAGCGGCG-----CTGGCCCTCTCG 684
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
346 CysTrpAsnSerLysProArgAsnArgProSerPheArgGlnIleLeuLeuHisLeuAsp 365
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
685 GTGTGAGCAGATGAAGAGCCGACTTTTCCACCTTCATGTATGAACTGTGCTGGG 744
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
366 IleAlaSerAla-----AspValLeuSerThr 374
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
745 AAGCAGACAGCTTCTTCTATCCAGGGCCAG-----GAGTAC 783
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
375 ProGlnLeuThrTyPheLysSerGlnAlaGluTrpArgGluGluValLysLeuHisPhe 394
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
784 ACCGTGCTTTTGGGATGGA----- 804
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
395 GluLysIleLysSerGluGlyThrCysLeuHisArgLeuGluGluLeuValMetArg 414
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
805 ---AAGAGGATCCAGAAC----- 822
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
415 ArgArgGluGluLeuArgHisAlaLeuAspIleArgGluHisTyrGluArgLysLeuGlu 434
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
823 -----TACAGGTGTGAACACA-----GAG 843
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
435 ArgAlaAsnAsnLeuTyrMetGluLeuAsnAlaLeuMetLeuGlnLeuGluLysGlu 454
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
844 AAGGGCTCATGAGGTGCAGAGATGTGC-----TGCCCTGGGATGAAGGTGAGC 894
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
455 ArgGluLeuLeuArgArgGluGlnAlaLeuGluArgArgCysProGlyLeuLeuLys-Pr 474
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
895 TGCCAGCTCCAGTCCAGAGATCCCTGTGGACAGCCCGAGGACCAAGAAATCTACATC 954
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
474 HisProSerArgGlyLeuLeuHisGlyAsnThrMetGluLysLeuLysLysArgAs 494
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
955 TACACCTCAAGGGCATGTGCCCTTAAACACACCCAGGCTTGGATCTCCAGCT 1014
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
494 nValProGlnAsnLeuSer-----ProHisSerGlnArgProAspIleLeuLysAl 511
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
1015 GTGTGACCTGCTTCTTGCCCTGCTGTTATTAAGAAGATTCCTACCTGGCTTAGCG 1074
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
511 aGluSer-----LeuLeuProLysLeuAspAlaAl 521
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
1075 GGCCTCGCCGATGGCTGTGGCTGTGTTTCCGTGGTGGCGGCAACCCAAAGGACAGC 1134
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
521 aLeuSerGlyValGlyLeu----- 527
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
1135 TGTCTCTACTGTCTCACACACAGCCCAAGTCCAAAGTTCAGCATCGCGGATGAAGAC 1194
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258
528 ---ProGlyCysProLysAlaProProSer---ProGlyArgSerArgGlyLysTh 545
   ::::::::::::::::::::-ValysIleSerAspPheGlyThrSer 258

1195 GCACGGCAGAACCCCTACCAGTGAAGGCATGAGGTGCTCAACAGCGGCTCTGAGTTC 1254
   ::::::::::::::::::::-LysAlaSer 553
545 rArgHieArg-----
1255 TGGTACAGCAATGGCGCGGCTCTTGTTCATCGACTGTGCTCCCTCGGAGATCTGCAGG 1314
   ::::::::::::::::::::-LysAlaSer 553
553 sGlySerCysGlyAspLeuProGlyLeuArgThrAlaValProProHisLeuProGly 573
   ::::::::::::::::::::-LysAlaSer 553
1315 CGGCTGGAGCCCT-----ACATGGCCCC-----CCTCCATG 1344
   ::::::::::::::::::::-LysAlaSer 553
573 yProGlySerProGlyLeuGlyGlyProSerAlaTrpGluAlaCysProAla 593
   ::::::::::::::::::::-LysAlaSer 553
1345 GTTACGT-----CA 1353
   ::::::::::::::::::::-LysAlaSer 553
593 aLeuArgGlyLeuHisAspLeuLeuArgLysMetSerSerSerSerProAspLe 613
   ::::::::::::::::::::-LysAlaSer 553
1354 CTCGTGTGCTGCTGAGGGCAGGAGGAGGAGTCTGTGTGCTGCTG-----ATGAC 1407
   ::::::::::::::::::::-LysAlaSer 553
613 uLeuSerAlaAlaLeuGlySerArgGlyArgGlyAlaThrGlyGlyAlaGlyAspProG 633
   ::::::::::::::::::::-LysAlaSer 553
1408 AAGGCCACTCTTGGTGTATGATACCTCCACCTACACCTACAGCTGTGTGCGCGTACTTC 1467
   ::::::::::::::::::::-LysAlaSer 553
633 ySerProProProAlaArgGlyAspThrProProSerGluGlySerAlaProGlySer 653
   ::::::::::::::::::::-LysAlaSer 553
1468 TCGC-----GGTCCCGCCAGCCCTCAGGACATGTTTCCC 1503
   ::::::::::::::::::::-LysAlaSer 553
653 rSerProAspSerProGlyGlyAlaLysGlyGluProProPro-----Pr 668
   ::::::::::::::::::::-LysAlaSer 553
1504 GTGCGGCCCTTGGACAGCAACC----- 1526
   ::::::::::::::::::::-LysAlaSer 553
668 oValGlyPro-GlyGluGlyValGlyLeuLeuGlyThrGlyArgGluGlyThrSerGlyA 688
   ::::::::::::::::::::-LysAlaSer 553
1527 -----CCCGCAGCCAGCCACACCGCC----- 1548
   ::::::::::::::::::::-LysAlaSer 553
688 rgGlyGlySerArgAlaGlySerGln-HisLeuThrProAlaAlaLeuLeuTyrArgAla 707
   ::::::::::::::::::::-LysAlaSer 553
1549 -----AACCAGAGTGTGCTGAGGGGACTCCATC 1578
   ::::::::::::::::::::-LysAlaSer 553
708 AlaValThrArgSerGlnLysArgGlyIleSerSerGluGluGluGlyGluValAsp 727
   ::::::::::::::::::::-LysAlaSer 553
1579 CGGACGTGAGCATCATGTACAGTGGAGGAGCTGGCAGCAGATCTGTATCCACAGGAA 1638
   ::::::::::::::::::::-LysAlaSer 553
728 SerGluValGluLeuThrSerSerSerGlnArgTrpProGlnSerLeuAsnMetArgGln 746
   ::::::::::::::::::::-LysAlaSer 553
1639 TCACTCACTGACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1698
   ::::::::::::::::::::-LysAlaSer 553
747 -----SerLeuSerThrPheSerSerGluAsnProSerAspGlyGlu 760
   ::::::::::::::::::::-LysAlaSer 553
1699 AGTTCCTCCCTCAAGCTCCCGAGCTCCCGAGCAGTCTCTCCAGTGTGCTTCTCCACC 1758
   ::::::::::::::::::::-LysAlaSer 553
761 GluGlyThrAlaSerGluPro---SerProSerGlyThrProGluValGly---SerThr 778
   ::::::::::::::::::::-LysAlaSer 553
1759 CACTGCGAGGACTCAGACATGCTACATACCGCGGTGCTGCTCCCGACAGGTCTGAGCAT 1818
   ::::::::::::::::::::-LysAlaSer 553
779 AsnThrAspGluArgProAspGluArgSerAspMetCysSerGlnGlySerGluIle 798
   ::::::::::::::::::::-LysAlaSer 553
1819 GACTGACCCCGCATGGAGCGGAG 1842
   ::::::::::::::::::::-LysAlaSer 553
799 ProLeuAspProProProSerGlu 806
   ::::::::::::::::::::-LysAlaSer 553

RESULT 4
US-09-345-473E-19
; Sequence 19, Application US/09345473E
; Patent No. 6558903
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin
; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof
; FILE REFERENCE: 35800/183781
; CURRENT APPLICATION NUMBER: US/09/345,473E
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
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LENGTH: 394
TYPE: PRT
ORGANISM: Homo sapiens
9-345-473E-19

nment Scores:
. No.: 2,63E-13 Length: 394
e: 279.50 Matches: 87
ent Similarity: 46.05% Conservative: 47
Local Similarity: 29.90% Mismatches: 108
Y Match: 6.89% Indels: 50
Gaps: 9

9-836-392-8_COPY_22_2205 (1-2184) x US-09-345-473E-19 (1-394)

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33 ArGHISAgPrOAspGluAAspIleSerGlnThrIleGluAAsnValArgGlnGluAlaLys 52
|||||
67 ATGCTGCACGGCGTCGACGACCCCTGCATCGTGGCGCTCATCGGCATCAGCATCCACCCG 126
|||||
53 LeuPheAlaMetLeuLysHisProAsnIleIleAlaLeuArgGlyValCysLeuLysGlu 72
|||||
127 -----CTGCTGCTGGCCCTGGAGCTCGCGCGCTCAGCAGCTCAACACCGTCTGTCTC 180
|||||
73 ProAsnLeuCysLeuValMetGluPheAlaAArgGlyGlyProLeuAAsnArgValLeuSer 92
|||||
181 GAGAACGCCAGAGATTCCTCTTTATACCCCTGGGACATGCTCACCCAAAAATA--- 237
|||||
93 -----GlyLysArgIleProProAspIleLeu 101
|||||
238 -----GCCTACGAGTCGCTCGGGCGCTGGCTACCTGCACAGAAA--- 279
|||||
102 ValAsnTrpAlaValGlnIleAlaAArgGlyMetAsnTyrLeuHisAspGluAlaIleVal 121
|||||
280 AACATCATCTTCTGTGACCTGAAGTCGACCAACATCTCGTGTGTGTCCTCCTT----- 330
|||||
122 ProIleIleHisArgAspLeuLysSerSerAsnIleLeuIleGlnLysValGluAAsn 141
|||||
331 ---GAGCTCAAGGACACATCAACATCAAGCTATCTGACTACGGGATTCGAGCAGTCA 387
|||||
142 GlyAspLeuSerAsnLysIle---LeuLysIleThrAspPheGlyLeuAlaArgGluTrp 160
|||||
388 TTCATATGAGGGCGCCTAGGCGTGGAGGGCACTCTCGCTACCGCCCGCCAGAGATCAGG 447
|||||
161 HisArgThrThrLysMetSerAlaAlaGlyThrTyrAlaTrpMetAlaProGluValIle 180
|||||
448 CCTCGCATGTATATGATGAGAAGTATATCTCTCTATGGAATCGTCTCTACGAG 507
|||||
181 ArgAlaSerMetPheSerLysGlySerAspValTrpSerTyrGlyValLeuLeuTrpGlu 200
|||||
508 TTGCTGTACGACAGCGCCCTGCATCGGGCCACCCACCACTCCAGATTGCC----- 558
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201 LeuLeuThrGlyGluValProPheArgGlyIleAspGlyLeuArgValAlaTyrGlyVal 220
|||||
559 -----AAGAAGCTGTCCAAGGGCATCCGCCCGGTCTCGGGCACCCCGAGGAAGTCAG 612
|||||
221 AlaMetAsnLysLeuAlaLeuProIleProSerThrCysProGluPro----- 236
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613 TTCGGCGGACTCGAGCGCTCATCATGGATGTGGGACACTAAGCCAGAGACGCGACCG 672
|||||
237 -----PheAlaLysLeuMetGluAspCysTrpAsnProAspProHisArg--- 252
|||||
673 CTGGCCCTCTCGGTGGTGAAGCAGATGAGAGACCCGACATTTTGGCCACCTTCATGTATGAA 732
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253 -----ProSerPheThrAsnIleLeuAspGln 261
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733 CTGTGCTGTGGGAAGCAGACAGCTTCTTCTC-ATCCAGGGCCAGGAGTACACCGTGT 791
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262 LeuThrThrIleGluGluSerGlyPhePheGluMetProLysSerPheHisCysLeu 291
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792 GTTTTGGGATGAAAGAGGATCCAGGAATA 824
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Db 282 ClnAspAntPrlyshHisGluLeGlnGluMet 292

RESULT 5
US-09-252-991A-30843
; Sequence 30843, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30843
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30843

Alignment Scores:
Pred. No.: 2,42e-12 Length: 663
Score: 268.00 Matches: 166
Percent Similarity: 28.89% Conservative: 40
Best Local Similarity: 23.28% Mismatches: 243
Query Match: 6.58% Indels: 264
DB: 4 Gaps: 32

US-09-836-392-8 COPY 22 2205 (1-2184) x US-09-252-991A-30843 (1-663)

QY	2170	TGCAGCTCTCAGCGCCGACGCTCCTCTAGACTGTAGAAATGT-----	2123
Db	144	CysCysTrpProAlaProAlaProAlaProAlaSerAlaGlyArgAlaCysCysAlaSerPro	163
QY	2122	-----CGAATCTCCTCGGCCGCCACGCCCC---TCCAGACGCCAGGCACCACT	2078
Db	164	AsnArgAaGArgArgGluProTrpProProSerProTyrAlaSerArgAlaGlyProAla	183
QY	2077	CTGTGTTTTCATTTTAAAGTGCACACACAGTGTCTTTGCCACCGCAGCATCCA	2018
Db	184	SerCysGlyArgProProAlaCysSerProValAlaThrAlaProThrAlaThrCysSer	203
QY	2017	CCAGCACCCCATGCGGAGTCAGCTCTCGGCTTTTAAGACGGCAATGACTCGGCCCGCT	1958
Db	204	Pro---ProSerAlaArgSer-----	209
QY	1957	GGGCTTCAGATTCCTTCAGGCCAATGACGATAACATCTCCACCGGCTCTGGGACCC	1898
Db	210	-----	213
QY	1897	AAATGAGTCTCTGACGGCGAGGATCTTCACGCGCTGCGAGGTCTGGCTGAAGTCTCCC	1838
Db	214	CysAlaCysAlaLysAlaValGlySerAlaAaG-----	224
QY	1837	CGTCCATGGGGGTGAGTCTATGCTCAGACCTGTGCGAGGCAGCACCGGCGGTATGTAGCA	1778
Db	224	-----	224
QY	1777	TGTCGATCTCTCCAGTCCGTGGAGAAAGGCACACTGGAAGAACTTCTCTGGGAGCTGG	1718
Db	225	-----SerProAlaAsnAlaTrpProAlaAla-----SerAlaTrp	236
QY	1717	GGAGCTTGAGGGGACCTGGCAGCTTCGCGGGGTGGGATGAGGAGTAGGAGGACATGG	1658
Db	237	CysProThrCysAsnSerAlaAaArgProSerAlaIleAlaSerThrAlaArgArgSerPro	256
QY	1657	AGCAGTAGTGTAGTGTATTCCTGTGTGATCAGGATCTGCTGCGCCAGCTCTCTCCTGT	1598
Db	257	SerThrAsn-----GlyArgProAlaAlaCysProThr-----	267


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1597 ACATGATGCTCAGGTCGGGATGGAGTGCCTCCCTCAGGACACCTTTGGGTGGCCGTGGC 1538
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268 -----ThrProAlaAsnAlaProAlaSerAlaAlaAsnTrpProTyr 285
1537 TGCGCTCCGGGGTTCGGGTGCCAGGCGCGACGGGAACA-----TGCCCC 1490
286 LysAlaProSerProAlaMetProSerThrSerAlaThrArgLeuAlaCys--- 304
1489 TGAGGGGGTGGGACCCCGCAGAGTACCGGCACACAGTGTGTAGTGGTGGAGTGGT 1430
305 -----GlyHisAspGlyAspAlaGlyArgAlaSerGlnThrProTyrArgAsp 320
1429 ACATCACCAGGAGTGGCTGTGTCATCCAGGCACACAGCAGCTCCTCCCTCGCCCT 1370
321 ThrSerProCysValProAsnCysValAsnTrpArgArg-----IlePro 336
1369 CAGAGTCGACACGACTGACGTAACCAATGG----- 1340
337 TpsrAlaValAlaLysThrSerProTyrProArgTyrProGlyMetProAlaGlyPro 356
1339 AGGGGCCATGTAGGCTCCAGCCCGCTGCAGATCTCCAGGAGGCACAGTCGATGCAA 1280
357 ArgProSerCysThrAlaValAlaAlaTrp---AlaProAlaArg----- 370
1279 GGAGGC-----CCGCCCATTTGCTGTACC----- 1256
371 GlyGlyTyrAlaAlaProArgAsnSerCysSerAlaGlyArgLeuArgArgVal 390
1255 AGACCTCAGAGCGGTGTGACCACTCCATGGGCT----- 1220
391 ArgArgSerAlaArgAlaTrpArgProTyrProAlaGlyArgAlaThrProAlaSer 410
1219 -----TCAGTGGTAGGGTCTCGCGTCTCTCATCCGCGA 1181
411 AspAlaArgArgAspSerAlaSerArgGlyArgProAlaThrAlaAlaAspHisPro--- 429
1180 TGCTGAACCTTGGACCTGTGGCTGTGTGAGCAGCAGGTAGGACAGCTGTCTTTGGGG 1121
430 -----AlaAlaTrpValSerAlaAlaArgArgThrSerSerAlaProIleAla 445
1120 TGCCCGCAGCAGGGAA---ACACAGCCCAAGCCCAT-----CGCGCA 1079
446 GlySerAlaProGlySerGlyThrAlaProArgCysHisProValArgLysAspGlyAla 465
1078 GGCCCGCTAAGCAGGTAGGAATCTTTTAATAACAGCAGCGCCCAAGAGCAGTGA 1019
466 GlyProAlaSerThrGlyArgSerArgArgTrpAlaAlaProAlaArgArgAla 485
1018 CGACAGCTGGAGTATCCAGGCTCTGGGTGTGTTTAAGGGGCACATGCCCTTGAGGG 959
486 Arg----- 486
958 TGTAGATGTAGATTTTCTGGTCTCGGTGGTGTCCACAGGATCTCTGGACCTGGAGCT 899
487 -----ThrGlyIleArgArgThrAlaAla 494
898 GGCAGCTACCTTCTCCAGGCGCAGCACAATCTCTGCACCTCCATGAGGCCCTTCTCTG 839
495 AlaAla----- 496
838 TGTTACACACCGTGTAGTTCCTGGACTCTCTTTCCATCCCAAAACACACCGGTGACT 779
497 CysTyrProPro-----ProAlaProGlyArgArgThr 507
778 CTGGCCCTGGGATGAGAAGAGGTCTGTCTCCACAGCAGCATGTTTCATCATGAAGG 719
508 ProAlaAlaArgArgSerAlaArgThrAlaProArgProAlaIleProAlaHisArg 527
718 TGCCAAATCGGGCTCTTCATCTCGCTCACCAGCAGGCGCAGCGCTCGCTTCTCTG 659
528 -----ProSerAlaSerAlaThrGlyTrpPro-----GlyProAlaLeuAla----- 541
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658 GCTTAGTGTCCAGC-----ACTCCATCATGAGCGCTGCGAGTGGCC 617
542 -----CysProAlaAlaAlaGlyArgArgProSerProAlaProAlaProAla 559
616 GGAACCTGCACCTCTCCGGCT---GCCCGAGAACCGGGCGGATGCCCTTGCACAGCTTCT 560
560 ProHisAlaArgProAlaGlyProAlaArgArgProGlyArgSerProAlaThrAlaPro 579
559 TGGCAATCTGGAGTGTGGTGGCCAGTGCAGGCG-----GCTGCTCGACAGCA 509
580 AlaAlaPheAlaAlaProAlaGlyProThrProAlaArgProProAlaAlaAlaThrGly 599
508 ACTCGTAGAGCA-----CCATTCCATAGAGACATATCTACCTTCTCATATATA 458
600 ArgProSerAlaProProAlaArgArgValArgTrpProTyrArg----- 617
457 CAATCGAGGCTGATCTCTGGGCGCTGGTAGCAGGAGTGCCTCCACGCTAGGCGC 398
618 -----SerAlaArgCysSerProAlaArgProThr 627
397 CCTCATGGAATGACTGCTCGAATCCGCTAGTGCAGTAGCTTGATGTTGATGCTCCT 338
628 ProArgSerAlaProGlyAlaAlaThrGlyAla----- 638
337 TCAGCTCAAGGACACACACAGAGATGTGCTCCGACTTCAGGTCCACAGAGATGATGTTT 278
639 -----ProThrGlyAlaAlaArgProArgArg 648
277 TCTTGTGAGTAGGCGCAGGCGCGAGCTGCTGGTAGG 239
649 ArgAlaAlaAlaProGlyLysArgArgSerAlaArg 661

RESULT 6
US-08-205-018-2
; Sequence 2, Application US/08205018
; Patent No. 5554523
; GENERAL INFORMATION:
; APPLICANT: Reddy, Usharani R.
; TITLE OF INVENTION: No. 5554523el Protein Kinase, Nucleic Acid
; TITLE OF INVENTION: Sequences Encoding the Same and Methods Related
; TITLE OF INVENTION: Thereto
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSEE: No. 5554523ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/205,018
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaumont, Rebecca R.
; REGISTRATION NUMBER: 35,152
; REFERENCE/POCKET NUMBER: CH-0488
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 668 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

09-836-392-8

Inment Scores:

1. No.: 2,9e-12 Length: 668
 re: 267.00 Matches: 139
 ent Similarity: 34.86% Conservative: 67
 Local Similarity: 23.52% Mismatches: 206
 y Match: 6.58% Indels: 179
 Gaps: 26

09-836-392-8_COPY_22_2205 (1-2184) x US-08-205-018-2 (1-658)

28 GCATCAAGAACTTCTCCGAGTTCGGCAG---GAGGCCAGCATGCTCCAGCCGCTCCAG 84
 150 AlavalysValArgAspLeuLysGluThrAspIleLysHisLeuArgLysLeuLys 169
 85 CACCCCTGATGTCGCGCTCATCGCATCAGCATCCACCGCTCTGCTTCGCC----- 138
 170 HisProAsnIleIleThrPheLysGlyValCysThrGlnAlaProCysTyrCysIleLeu 189
 139 CTGGAGCTCGCGCGCTCAGAGCCTCAACACCGCTGCTGCCGAGAACGCCAGAGATTCT 198
 190 MetGluPheCysAlaGlnGlnLeuTyrGluValLeuArgAlaGlyArg----- 206
 199 TCCTTTATACCTCGGGACACATGCTCACCCAAAATAAGCTACCAGATCGCTCGGC 258
 207 -----ProValThrProSerLeuLeuValAspTrpSerMetGlyIleAlaGly 223
 259 CTGGCTTACTCTGACAAAGAAACATCATCTTCTGTGACCTGAAGTCGCAACAATTCTG 318
 224 MetAsnTyrLeuHisLeuHisLysIleIleHisArgAspLeuLysSerProAsnMetLeu 243
 319 GTGTGTCTTCACTCAAGAGACATCAACATCAAGCTATCTGATCATCGGATTCG 378
 244 IleThrTyrAspVal-----ValLysIleSerAspPheGlyThrSer 258
 379 AGGCAG---TCATTCCATGAGGCGCCCTAGCGTGGAGGCACCTCCCTGCTACAGGCC 435
 259 LysLeuSerAspLysSerThrLysMetSerPheAlaGlyThrValAlaTrpMetAla 278
 436 CCAGATCAGCGCTCGCATGTPATGATGAGAGAGTAGATATCTTCTCTATGGAATG 495
 279 ProGluValIleArgAsnGluProValSerGluLysValAspIleTrpSerPheGlyVal 298
 496 GTGCTCTACAGTGTGTCTCAGACAGCCCT----- 528
 299 ValLeuTrpGluLeuLeuThrGlyGluIleProTyrLysAspValAspSerSerAlaIle 318
 529 -----GCACTGGCCACCACCACTCCAGATTGCCAAGAAGCTGTCCAAGGCGCATCCGC 582
 319 IleTrpGlyValGlySerAsnSerLeuHisLeu----- 329
 583 CCGTTTCTGGGCGAGCCGGAGGAGTGCAGTTCGCGGACTCGAGCGCTCATGATGAG 642
 330 ProValProSerSerCysProAsp-----GlyPheLysLeuLeuLeuArgGln 345
 643 TGCTGGGACACTAAGCCAGAGAAGCCAGCG-----CTGCCCTCTGTCG 684
 346 CysTrpAsnSerLysProArgAsnArgProSerPheArgGlnIleLeuHisLeuAsp 365
 685 GTGTGAGCCAGATGAAGGACCCGACTTTTGGCCACTTCATGTATGAAGTGTGCTGGG 744
 366 IleAlaSerAla-----AspValLeuSerThr 374
 745 AAGCAGACAGCTTCTTCTCATCCAGGCGCAG-----GAGTAC 783
 375 ProGlnGluThrTyrPheLysSerGlnAlaGluTrpArgGluValLysLeuHisPhe 394
 784 ACCGTGGTGTTCGGATGA----- 804
 395 GluLysIleLysSerGluGlyThrCysLeuHisArgLeuGluGluValMetArg 414
 805 ---AAAGAGGAGTCCAGGAC----- 822

415 ArgArgGluGluLeuArgHisAlaLeuAspIleArgGluHisTyrGluArgLysLeuGlu 434
 823 -----TACAGGTGGTGAACACA-----GAG 843
 435 ArgAlaAsnAsnLeuTyrMetGluLeuAsnAlaLeuMetLeuGlnLeuGluLeuLysGlu 454
 844 AAGGCGCTCATGAGGTGCAGAGGATGTC-----TGCCCTGGGATGAAGGTGAGC 894
 455 ArgGluLeuLeuArgArgGluGlnAlaLeuGluArgCysProGlyLeuLeuLys-Pr 474
 895 TGCAGCTCCAGTCCAGAGATCCCTGTGGACAGCCACCGAGCCAGAGAAATCTACATC 954
 474 OHisProSerArgGlyLeuLeuHisGlyAsnThrMetGluLysLeuLysLysArgAs 494
 955 TACACCTCAAGGCGCATGTGCCCTTAAACACACACCCACAGCGCTTGGATATCTCCAGCT 1014
 494 nValProGlnAsnLeuSer-----ProHisSerGlnArgProAspIleLeuLysAl 511
 1015 GTCTGCTACCTGCTTCTTGGCGCTGCTGTTTAAAGAAATCTCTACCTGCTGTAGCG 1074
 511 adLuser-----LeuLeuProLysLeuAspAlaAl 521
 1075 GGCCTCGCGCATGGCTTGTGGCTGTGTTTCCGTGCTGGCGGCACCCCAAGGACAGC 1134
 521 aleuSerGlyValGlyLeu----- 527
 1135 TGCTCTACCTGTGCTACACACAGCCACACAGGTCCAAGTTCAGCATCGCGGATGAGAC 1194
 528 ----ProGlyCysProLysAlaProProSer---ProGlyArgSerArgGlyLysTh 545
 1195 GCACGGCAGAACCCCTACCCAGTCAGGCCATGAGGTGTCAACAGCGCTCTGAGGTC 1254
 545 rArgHisArg-----LysAlaSerAlaLy 553
 1255 TGCTACAGCAATGGCGCGGCTCTCTGTCATCAGCTGTGCTCCCTGGAGATCTGCAGG 1314
 553 sGlySerCysGlyAspLeuProGlyLeuArgThrAlaValProHisGluProGlyL 573
 1315 CGGCTGGAGCCCT-----ACATGGGCC-----CCTCCATG 1344
 573 yProGlySerProGlyGlyLeuGlyGlyGlyProSerAlaTrpGluAlaCysProAl 593
 1345 GTTACGT-----CA 1353
 593 aLeuArgGlyLeuHisAspLeuLeuArgLysMetSerSerSerSerProAspLe 613
 1354 GTCGTGTGAGCTCTGAGGCGAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1407
 613 uLeuSerAlaAlaLeuGlySerArgGlyArgGlyAlaThrGlyGlyAlaGlyAspProG 633
 1408 AAGGCCAACTCTCTGCTGATGTACCACTCCACCTCCAGCTGTGTGCTGCTGCTGCTG 1464
 633 ySerProProAlaArgGlyAspThrProProSerGluGlySerProProGlySerTh 653
 1465 TTCTGCGGCTCCCGAGC-----CCCTCAGG 1492
 653 rSerProAspSerProGlyGluProLysGly 663

RESULT 7

US-09-252-991A-26129
 ; Sequence 26129, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: ASRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190

R10R FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

Q ID NO 26129

LENGTH: 885

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

9-252-991A-26129

nment Scores:

. No.: 3,85e-12 Length: 885

e: 266.00 Matches: 218

ent Similarity: 31.68% Conservative: 50

Local Similarity: 25.77% Mismatches: 293

y Match: 6.53% Indels: 285

4 Gaps: 44

9-836-392-8_COPY_22_2205 (1-2184) x US-09-252-991A-26129 (1-885)

2161 CCAGCGCGCCAGCTCCCTAGGACTGGTAGAAGTTCGMACTCCTCGGCCCCAGC 2102

90 ProSerGlyProAlaProArgGlnArgVal----- 101

2101 CCTCCAGACGCCAGCCAGCCACTCTGTGTTTCATTTTCAAAGGTGCACACACAGTGT 2042

102 -----PheGlnArgAspArgHisArgPro 109

2041 CCTTTGCCACACGCCAGCAT-----CCACGACACCCCATGG 2003

110 GlyHisProAlaGlnGlnHisGlnGlyArgArgProLeuProProAlaArgProAla 129

2002 GAGTCAGCTCTCGGGCTTTAAGACGGCAATGACTCGGCCCGCTTCAAGATCCT 1943

130 GlnGluArgCysArgAlaValArgArg-----AlaGlyArgArgSerSer 145

1942 TCTCAGCGCCAAATGACGATAACATCTCCACGCGCCTGGGGACCCAAATGAGTCTCTGA 1883

146 AlaGlyGly----- 148

1882 CGGCAGAGATCTTCACGCGCTCCAGGTGCTGGCTGAAGTCTCCCGTCCATGGGGTCA 1823

149 ---ArgGlyMetGlyArgIleAlaLeuAlaGly-----GlnProArgProGluGly--- 164

1822 GGTATGTCAGACCTGTGCGAGGACGACCGCGCTATGTAGCATGTCTGAGTCTCTCG 1763

165 -----ArgArgGlnHisArgAsp-----ArgProGln 173

1762 AGTCGTGGAGNAAGGCACATCGAAGACTTGTCTGGG----- 1724

174 AlaAlaAlaHisArgAlaHisProTyrLeuArgAlaGlyProArgArgArgLeuValGln 193

1723 -----AGCTGGGGAGGCTTGGAG 1706

194 ProAspAlaProArgHisAspGluProGlyArgProArgCysHisArgGlyGlyProAla 213

1705 GGGAGCTGGAGCTCGCGGGGTGGGATGAGGAGTAGAGGACATGAGCAGTACTAG 1646

214 Gly-----GlnProGlyAlaLeuProArgSerValGlyArgProAlaGlySerProPro 231

1645 TGAGTGATTCCTGTGGATCAGGATCTGCGTCCAGCTCCTCACTGTATCATGATCTCA 1586

232 GlyLeuSerProAlaGlyGlnGly----- 239

1585 COTCGCATGAGTCCCTCCAGGCACCTTTGGTTGGCGTGTGGCTGGCTGCGCGGG 1526

240 GlnProArgArgGlnPro-----AlaProAlaGlyCysProArgArgGlnProProGly 257

1525 GTTCCGTCTCCAGGCGCCAGCGGAACA-----TGTCCCTGAGGGGCTGG 1478

259 GlyArgCysProArgProCysArgAlaLeuProGluProGlyGlnProGlyArgGlyAla 277

1477 GGACCCCGCAGAGTACCGG-----CACACAGCTGGTAGG 1442

278 AlaArgArgArgArgGlyProValArgArgProPheArgCysThrAlaLeuArgArg 297

1441 TGTGGAGTGTATCATCCCAAGGAGTTGSCCTTGTATCATCCAGGCACACAGACCTCT 1382
 QY
 298 GlnArgAlaAlaAlaLeuProArgSer-----ValAlaGlnArgAsnProAla 313
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 1381 CCTCTGCGCCTCAGAGCTGCACAGCTACACATTAACATGAGGGGGCCATGTAGGGCT 1322
 QY
 314 ProLeu-----ArgAlaAlaThrValAlaAlaGlyProAlaArgGlnArgHisArgArg 331
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 1321 CCAGCCGCTGCAGATCT-----CCAGGGAGGCACAGTCGATGACAA 1280
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 332 ProAlaArgLeuValGlyThrAlaArgProValProProAlaArgHisAlaAlaAla 351
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 1279 GGAGCGCGGCCCATCTGTCTACAGACCTCAGAGCGCTGTGTGACCACTCCATCGCT 1220
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 352 Gly-----ArgThrSerArgArg-----ProValPro 360
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 361 ArgLeuArgArgGlyArgHisArgProGlyIleAlaGlyArgLeuArgProProAla--- 379
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 QY
 380 -----AlaGlySerProGlyThrAlaValAlaGly---Pro 392
 Db
 1114 GCACCGCGGAAACACAG---CCACAAGCCATCCGCGAGGC-----CCGCTA 1070
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 393 AlaGlnArgProAlaAlaGlyAlaAspAlaHisLeuAspGlyLeuArgLeuArgProAla 412
 Db
 1069 AGACCGAGTAGGATCTTTTAAATACAGCGACCGCCCAAGAGCAGGTGACGA----- 1016
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 413 ArgProGlyProAspHisValAlaValGluSerArgProGluAlaAspProArgProAla 432
 Db
 1015 -----CAGCTGGAGTAT 1004
 QY
 433 ArgArgArgProGlyArgHisAlaGlyAlaArgProProAlaAlaArgProGluArg 452
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 453 ProAlaProGlyThrGlyAlaCysGlnProAlaMetAlaAlaGlyThrArgPro----- 470
 Db
 958 TGTAGATGTAGATTTCTGCTCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 999
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 898 GGCAGCTCAGCTTCATCCAGGCGACACATCTCTGCACCTCCATGAGGCCCTTCTCTG 839
 QY
 491 GlyTyrGlyProAspArgProAlaSerArgArgThrAla-----GlyTyrLeu 506
 Db
 838 TGTTTCAACCGCTGTAGTCTCTGAGTCTCTTTTCCATCCCAAAACACACCGGTGACT 779
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 507 AlaGlyProValAlaAlaGlyArgProGlnProPheArgProGluHisPro-----Ala 524
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 778 CTTGGCCTGGAGT-----AGAGAAGGCTGTCT 749
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 525 AspGlyGlyGlyArgLeuArgThrSerArgAlaLeuAlaLeuProArgArgArgAlaAla 544
 Db
 748 GCTTCCACAGCAGCAGTTTATCATCAATGAAGGTGCAAAAGTCGGTCTCTCATCTGGCTCA 689
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 545 ValProHisGlySer-----ArgAlaProGlySerGlyGlu 556
 Db
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 557 ArgGlnAlaGlyProGlyAlaArgArgArg----- 567
 Db
 628 CCTGCAGTCCCGGAACCTGACCTTCTCGGCTGCGCCAGAACCGGGCGGATGCCCTTGG 569
 QY
 568 -----AlaGlnArgAlaCysProAlaAlaArgProArgProAspLeuValArgAla 584
 Db
 568 ACAGCTTCTTGGCAA-----TCTGGAGCTGGTGGC 536
 QY
 585 ThrAlaLeuArgGlnProAlaHisArgArgThrLeuValGluArgAlaAlaGlyGly 604
 Db


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124 ArgSerPheProAlaLeuMetMetArgProCysTrpProLeuSerMetArgLeuAlaSer 143
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
287 TCTTCTGTG-----ACCTGAAGT 304
144 SerSerLysProCysTrpLeuGluIleSerProTrpArgLeuSerArgThrPheSer 163
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
305 CGGACAACTTCTGGTGTGCTCCCTTGACG-----TCAAGGAGC 343
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
164 ArgSerMetLeu---SerGlyProArgAlaLeuIleArgProProTrpLeuSerArgSer 182
344 ACATCAACATCAACCTATCTGACTACGGATTCGAGGCAGTCATTCATCAGCGGCGCC 403
183 ProProArgArgSerArgLeuThrPro-----ArgSerPro 194
404 TAGCGCTGGAGGCACTCTCTGGCTACAGCGCCCGACAGATCAGGCCTCGCATTTGTATAT 463
195 -----ThrSerArgProTrpArgCysThrArgArgSerThrVal 207
464 ATGAGAGGTAGATATGTTCTCTATGGAATGGTGCTCTACGAGTTGCTGTCCAGGACAGC 523
208 ArgArgArg-----SerProArgAlaGluIleSerProProSerAlaGluSerThr 284
524 GCCCTGCACTGGGCGCACCCACACTCCAGATTCGCAAGAGCTGCCAAGGGCATCGCC 583
225 ArgProAlaValSerSerSerProSerLeuValSerArgProProArgLeuSer--- 243
584 CGGTTCTGGGCGACCGGAGGAAGTGCATTCGCGCGACTGC-----AGCGCG 631
244 ArgLeuAlaAlaLeuArgArg-----SerArgCysLeuProLeuArgAlaPro 259
632 TCATGATCGGAGTCTGGGACATAACCCAGAGAGCGACCGCTGCCTGTCGGTGGTGA 691
260 ProArgLeuSerArgSerAlaLeuLeuThrSerSerThrProTrpLeuIleAsnTrp--- 278
692 GCCAGATGAAGGACCCGACTTTTGGCCACCTTCATGTATGAACATGTGCT---GTGGGAAGC 748
279 -----ProProSerAlaLeuSerSerAlaProValAlaThr 290
749 AGACAGCCTTCTTCATCCAGGGCCAGAGTACACCGTGG-----TGTTTT 796
291 LeuArgProAlaLeu---ProGluSerArgProLeuProLeuLeuSerArgGluAlaLeu 309
797 GGGATGGAAGAGGAGCTCCAGGAAT-----ACACGGTGTGTAACACAGAGAGGCGCC 850
310 AlaSerValArgAlaProGluThrValProSerAlaTrpLeuSerSerAlaProSer 329
851 TCATGGAGGTGCAGAGATGT-----GCTGCCCTCGGATGAAGG 889
330 ThrArgArgSerMetProAlaArgLeuAlaArgValProLeuAlaLeuLeuSerArgArg 349
890 TGAGGTGCGCACTCCAGGTCAGAGATCCCTGTGGACAGCACACCGAGG-----ACCAGA 943
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944 AAATCTACATCTACCCCTCAAGGCAATGTGCCCTTTAAACACACCCCAACAGG----- 997
370 AlaTrpAlaMetArgArgValArgLeuAlaAlaProIleArgArgProProArgLeuSer 389
998 -----CCTTGGATCTCCAGCTGCTGCTCACTGCT--- 1027
390 ArgLeuAlaAlaAlaArgValLysAlaArgSerLeuGluIleSerProAlaProLeu 409
1028 -----TCTTGG-----CCGTGCGCTG 1042
410 SerThrAlaProSerTrpArgSerSerSerAlaProGlyValAlaIleArgProProSer 429
1043 TTATTAAAAAGAAATCTACTCTGTGCTTAGCGGCGCTCGCCGATGGGCTGTGGCTGTGT 1102
430 ArgLeuThrSerValProProLeuArgSerArgValThrProValSerLeuThrArgThr 449
1103 TTCCCG-----TGTGCGGGGACCCCAAGGACAGCTGCTCTACCTGCTGCACACA 1156
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450	ProProProArgTrrpSerArgPropheArgLeuAlaSerSerArgProLeuAlaLeuThr	469
1157	CAGCAACAGAGTCCAAAGTTCAGCATCGCGATGAAGACGCAC	1198
470	ArgProCysTrrpProLeuSerSerArgAlaAlaThrArgValMetProAlaLeuLeu	488
1199	GCACGAACCCCTACCCAGTGAAGGCCCATGGAGCTGGAGCTGG	1234
489	ProMetProProLeuArgLeuLeuSerSerThrProVal	503
1235	TCACAGAGGGCTCTGAGGTCGTGTACA	1261
504	SerThrAlaProLeuAlaLeuIleThrProGluArgLeuLeuSerArgLeuAlaProCys	523
1262	GCAATGGCCGGGCTCTCTTGTTCATCGACTGTGCTCTCTCGAGATCTGCAGCGGGCTGG	1321
524	SerValThrProAlaSerLeuSerSerLeuProProTrrpLeuSerSerAlaAlaTrrp	542
1322	AGCCCTACATGG	1357
543	LeuValSerAlaSerAlaProAlaLeuGluLysValProProArgLeuSerArgArgAla	562
1358	TGTGAGTCTGAGGGCAGAGGGAGAGTGTCTGTGTGCTGTGATCAAGGCCCACT	1417
563	AlaArgAlaValArgLeuProSerLeuThrSerAlaProProTrrpLeuSerSerThrPro	582
1418	TGTGTATGTACACTCCA	1438
583	ProArgLeuThrLeuArgLeuPheTrrpLeuSerSerArgProProSerProLeuAsnSer	602
1439	CCACCTACCACTGTGTGCCGTACTTCTGGGGGTCCCAAGCCCC	1489
603	SerProProSerArgLeuArgProSerArgProAlaSerThrProLeuAlaTrrpPheSer	622
1490	GGGACATGTTTC	1531
623	ArgArgCysThrValArgArgProLeuSerProMetThrLeuProProArgLeuSer	642
1532	CAGCCAGCCACACGGCCAAACCCAAAGTGTCTGAGGGGACTCCATCGCGACG	1585
643	SerCysSerArgAlaPheThrAlaThrPheGluValLeuGluIleSerProAlaArgLeu	662
1586	TGAGCATCATGTACAGTGTAGAGCTGGGCAGCCAGATCTGTATCCACCAGAACTCATCA	1645
663	SerThrCysArgAlaSerIleAlaMetProProPheAlaAlaIleSerGl	679
1646	CTGACTACTGTCCATGTC	1684
679	nasPTrpLeuSerIleValSerAlaAlaThrPheArgValPheSerLeuThrSerSe	699
1685	CCGCCA	1711
699	rProProCysTrrpAlaArgLeuProSerValAlaCysArgSerProLeuAlaAlaIleAr	719
1712	GCTCCCGACGTCGCCAGAGTCTT	1738
719	gProProAlaLeuProThrAlaPheAlaAlaSerArgArgProSerLeuAsnSerLe	739
1739	CCAGTGTGCTTTCTCCACGACTGCGAGGACTCAGACATGCTACATACGCCCGGT	1794
739	uProProTrrpSerLeuArgLeuAlaThrSerThrArgThrProAlaLeuProLeuAl	759
1795	GCTGCTCGAGAGTCTGACATGACCTGACC	1828
759	AlaLeuProProSerArgLeuSerLysAlaProProValAlaLeuLysProAlaSerAlaTh	779
1829	CCATGGACG	1837
779	rSerThrProProArgLeuSerArgLeuAlaProTrrpPheAsnSerLeuArgLeuAs	799
1837		1837
799	pSerArgProProAlaArgLeuSerSerCysProThrValThrArgCysAlaProTrrpLe	819

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1838 -----GGAGACCTTCACCCAGCCACTGCGCGCGTG 1869
819 userArgLeuProSerSerArgLeuSerSerArgProArgLeuThrSerArgProPr 839
1870 AAGA-----TCTCGCGC----- 1882
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1883 -----TCAGAGACCTCATT 1896
859 gleuAlaAlaGluAsnLysProArgLeuSerMetAlaProLeuAlaThrThrSerAr 879
1897 TGGTCCCGGCGCGGTGGAGATGTTATCGTATTCGCTGCGGTGGAGAGGATTCGAGCC 1956
879 gSerPro-----IleSerLeuProProArgLeuSerArgLeuPr 893
1957 CAGCGGCGCGGAGTCA---TTGCCGTCTTAAAGCCCGAGAGCTGACTC----- 2002
893 oThrArgAlaSerThrArgLeuProGluThrSerProSerProArgLeuThrSerAlaTr 913
2003 -----CGCATGGGTGCTGTGG---ATGCTGCCGTGGTGGCAAGGACACTGTT 2049
913 pAlaLeuThrArgValAspCysTrpLeuProSerArgProCysTrpProLeuSerSerVa 933
2050 GTGTGCACCTTTGAAATGAAACACAGAGTGTGCTGCCGCTCGAGGGCTGGGGC 2109
933 lAlaAlaProThrSerArgSerPheArgProIleThrTrpProArgLeuSerArgSe 953
2110 GCAGGAGTTCGACATTTTACCAGTCTACGAGAGCTGGCGCGCTGGAGGCTTC 2169
953 rProArgValLeuThrThrAlaArgSerArgLeuCysAsnArgProSerTrpArgLeuSe 973
2170 A 2170
973 r 973

LT 10
19-252-991A-31760
Sequence 31760, Application US/09252991A
Accession No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31760
LENGTH: 1706
TYPE: PR1
ORGANISM: Pseudomonas aeruginosa
19-252-991A-31760

Inherent Scores:
i. No.: 2,02e-11 Length: 1706
e: 258.00 Matches: 201
ent Similarity: 32.66% Conservative: 57
: Local Similarity: 25.44% Mismatches: 259
y Match: 6.36% Indels: 273
4 Gaps: 43

19-836-392-8_COPY_22_2205 (1-2184) x US-09-252-991A-31760 (1-1706)
3 GCTGAGGACCTCGCGGCGCACCGATGCCATGAGAACTTCTCCGAGTTCGCGGAGGAGGC 62
1088 AlaArgAlaProAla---HisArg-----Pro 1095

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QY 63 CAGCATGTGTGCACCGGTGTGCAGCACCCCTGCATGCTGGCGCTCATCGGCATCAG----- 116
Db 1096 GlnArgProAlaProProAlaLeuProAlaThrArgArgLeuGlnArgAspArgArg 1115
QY 117 ---CATCCACCCGCT-----CTGCTTCGCCCT 140
Db 1116 ValHisProLeuAlaGlyLeuValArgArgThrArgArgArgArgArgLeuArgPro 1135
QY 141 GGAGCTCCGCGCGCTCAGCACCTCAACACCGTGTCTCCGAGAACGCCAGAGATTCTTC 200
Db 1136 ArgLeuArg---HisArgGluProGlyHisArgProLeuArgHisArgHisArgMetArg 1154
QY 201 CTTTATACCCCT-----GGGACACATGCTCACCACCAAAATAGCCTACCAGATCGC 251
Db 1155 ArgProLeuProProAlaAlaGlyThrArgProArgProGlyAsnLeuAlaThrLeuGly 1174
QY 252 CTCGGCGCTGCCCTACTCTGCACAGAAAAACATCATCTTCTGTGACCTGAAGTCGACAA 311
Db 1175 AlaAlaAlaGlyAspProAla-----ProProGlyPhe 1186
QY 312 CATCTGTGTGTGCTCCCTTGACGTCAA----- 338
Db 1187 LeuProGlyLeuValProArgArgArgGlnArgThrArgThrAlaAlaArgArgHisArg 1206
QY 339 -----GGAGCACATCAACATCAAGCTATCTGACTACGGGATTCGAGGCGCATCATT 389
Db 1207 GluGlyProGlyAlaGlnArg----- 1213
QY 390 CATTGAGGCGCCCTAGCGGTGGAGGCATCTCTGGCTACCA-----GGCCCCAGAGAT 443
Db 1214 -----GlyAsnProSerHisGlySerSerGlyLeuProMetSerGlyProLys-Va 1231
QY 444 CAGGCCCTCGCATTTATATGATGAGAAGTAGATATGTTCTCTATGGAATGTGCTCTA 503
Db 1231 l---ValArgIleValThrArgGluGluAla-lleAlaThr----- 1243
QY 504 CGAGTTGCTGTGAG-----GACAGCGCCCTG---CACTGGGCCACCA 542
Db 1244 -----CysGluArgAspLeuGlnArgLeuAspLysAlaLeuAlaArgTrpGluAsnG 1261
QY 543 CCAGCTCCAGATTGCCAGA-----AGCTGTCCAGGGCATCGCCCGCTTCTGGGCA 596
Db 1261 InAlaSerArgLeuAlaGlnLeuSerAspAlaGluArgAlaAlaAlaHis----- 1277
QY 597 GCCGAGGAAGTGCAGTTCGCCGCTGCTGAGCGCTCATGATGAGTGTGGGACACTAA 656
Db 1278 --AlaArgArgAlaSerLeuHisAlaLeuAlaArgThrGlyThrLeuAlaGlyArgAlaT 1297
QY 657 GCCAGAGAAGCGACCGCTGGCCCTGTGCGTGTGGTGGAGCCAGATGAAGGACCCGACTTTC 716
Db 1297 hrThrGlyGluAspArg-----LysArgIleP 1306
QY 717 CACCTTCATGTATGAACATGTGCTGTGGGAGCAGACAGCCCTTCTTCATCCCGAGGCCA 776
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Db 1326 roAlaThrProProProGlyLysArgGlnArgProAlaProGly----- 1341
QY 834 GAACACAGAGAAGCGCTCATGGAGGTGCAGAGATGTGCTGCCCTGGGATGAGGTGAG 893
Db 1342 --ProArgArgGlnAlaArgCysArgGlnArgGlySerProAla-----AsnProA 1358
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Db 1358 laSerAlaGlyArgArgArg-----ProProArgArgArgGlySerProA 1373
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1074	GGGCTCGCGATGGCTGTGGTGTGTTCCCGTGGTGGCGGACCCCAAGGACAG	1133
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1393	roAlaargThr-----ArgProAlaProGluAaspArgAsnAlaHisHisProGlyT	1411
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1411	hrValAlaAargProAlaThrGlyArgProAlaAargThrAlaProGlyAlaHisAargP	1431
1247	-----CTGAGGTCTGTGTCAGCAATGGCGCGGCTCTCTGTCATCGACTGTGCTC	1298
1431	roAlaHisAargThrAlaThrAlaAaAargArg-----	1442
1299	CCTGGAGATCTCGACGGCTCGAGCCCTACATGCCCCCTCCATGTTAGTCAGTCGT	1358
1443	-----GlyGlnAArgProSerValPro-----	1449
1359	GTGCAGCTCTGAGGCGAGGAGGAGTGTCTGTGTCGTGATGACAGGCCAACTC	1418
1450	-----ArgAlaThrGlyThrArgAargSer-----ArgThrAlap	1461
1419	CTTGTGTGATGTACCACTCCACCACTACCACTGCTGTGCTCCCGT-----	1462
1461	ro-----GlyAlaProGlnProAlaAlaAargGlnProGlyProAargProArgProG	1478
1463	-----ACTTCTGGGGTCCCGAGCCCTCAGGACATGTTCCCGTCCGCGCC	1511
1478	lyAargProAargThrProAlaAlaThrProAlaPro---GlyThr-----ProAlaAargP	1495
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1515	rgArgLeuProAlaAArgGlnAArgSerAlaAlaThrArgThrHisArg-----	1531
1626	GATCCACCGAATCACTCACTGACTGACTGCTCCATGCTCTCTACTCTCTCATCCCAAC	1685
1532	--AlaMetGlnAArgHisProHisAargProProProAlaThrGlyAargProArgProP	1551
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1721	-----GCTCCCAAGCAAGTCTTCAGTGTGCTTCTCCACCGACTCGGAGGATC	1772
1571	rgLeuGlyAlaAaspArgGlnGlyAargPro-----AlaGlnThr-----	1583
1773	AGACATCTACATACGCGCGGTCTGCTCCCTCCGACAGGTCTGAGCATGACCTGACCCCAT	1832
1584	ArgHisProArg-----LeuAarg-----ProGlySerArg	1593
1833	GGACGGGAGACCTTCACGACAGCACTCGAGCGCGTGAAGATCTTCGCGGTGAG-----	1889
1594	ArgGlnGlyAargGlnAargProProAlaThrAlaAargAargProGlnAargGlnProA	1613
1890	CCTCATTTGGTCCCAAGCGCGGTGAGATGTTATCGTCAATGGCTGGAGAGGATTC	1949
1614	GlnProAlaAargProAargHisAargAsnProLeuValAargValPro-----	1629
1950	TGAAGCCAGCGGCGCGAGTCAAT-----TGCGGTCTT	1982
1630	---ThrProProGlyProAlaAaAargProGlyAargArgThrGlnAargGlyThrAla	1648
1983	AAAGCCCGAGAGCT-----GACTCCGCA	2006

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1649 GlyGlyGlyArgSerGlyValGluGlyAaspTrpArgGlyArgAlaAlaGlyAaspGlyGly

1668

QY

2007 TGGGCTGTGTGTGATCTCCGCTGGTGGCAAGGACACTGTTGTGTGACCTTTGAAA

2066

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1669 GlyAlaAlaGluGlyValValGlyGlyProAlaGlyAlaSerAlaAargHisSerIleArg

1688

QY

2067 TGAACACACAGAGTGGTGGCTGGC

2090

Db

1689 AlaValHisArgLeuThrProGly

1696

RESULT 11

US-09-345-473E-43

US-09-345-473E-43

Sequence 43, Application US/09345473E

Patent No. 6558903

GENERAL INFORMATION:

APPLICANT: Hodge, Martin

TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof

FILE REFERENCE: 35800/183781

CURRENT APPLICATION NUMBER: US/09/345,473E

CURRENT FILING DATE: 1999-06-30

NUMBER OF SEQ ID NOS: 62

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 43

LENGTH: 626

TYPE: PRT

ORGANISM: Homo sapiens

US-09-345-473E-43

Alignment Scores:

Pred. No.: 2,13e-11

Length: 626

Score: 255.50

Matches: 150

Percent Similarity: 33.59%

Conservative: 71

Best Local Similarity: 22.87%

Mismatches: 242

Query Match: 6.30%

Indels: 193

Gaps: 28

US-09-836-392-8_COPY_22_2205 (1-2184) x US-09-345-473E-43 (1-626)

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4 CTGAGGACCTGCGGGCCAGCCGATGCCATG-----AAGAAC

39

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74 ValArgHisAargGlnSerGlyGlnValMetValLeuLysMetAenLysLeuProSerAsn

93

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40 TTCTCCGAGTTCGGCAGGAGCCAGCATGCTGCGCGTGCAGCACCCTGCTGCTGCTG

99

Db

94 ArgGlyAasnThrLeuArgGluValGlnLeuMetAasnArgLeuAargHisProAenIleLeu

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159

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114 ArgPheMetGlyValCysValHisGln-----GlyGlnLeuHis

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210

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127 AlaLeuThrGluTyrMetAasnGlyGlyThrLeuGluGlnLeuLeuSerSerProGluPro

146

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211 CTGGGACATGCTCACCACCAAAATAGCTACCATGCTGCGCTGCGCGCTGCTGCTGCTG

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432

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492

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225 AlaProGluValLeuAargGlyGluLeuTyrAaspGluLysAlaAaspValPheAlaPheGly

244


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 552 -----ArgLeuHisSer-----AlaPr 557
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 591 oCys----- 592
 1837 GGGGAGACCTTCAGCGAGCCTGAGGCGGTGAAGATCCTCGCGG----- 1882
 593 -----ProGlyLeuGlnSerCysArgProLeuArgGlySerProLysLeuProAspPh 610
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 610 eLeuGlnArgSerProLeuProLeuLeuGlySerProThrLysAlaGlyProSerPh 630
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 630 eAspPheProLysThrProSerSerGlnAsnLeuLeuThrLeuLeuAlaArgGlnGlyVa 650
 1946 -ATTCTGAAGCCGAGGCGGCGAGTCAATGCGCTTTAAAGCCCGAGAGCTGACTCCG 2004
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 668 -----ProPheHisGlnGlnLeu----- 674
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 2125 ATTTCCTACAGT 2137
 691 rPheSerThrSer 695

Sequence 12, Application US/09266225D
 Patent No. 6573364
 INVENTOR INFORMATION:
 APPLICANT: Nardabalan, Krishan
 APPLICANT: Kingsmore, Stephen
 APPLICANT: Tchernev, Velizar
 TITLE OF INVENTION: Isolation and Characterization of Hermansky-Pudlak

TITLE OF INVENTION: Syndrome (HPS) Protein Complexes and HPS Protein-
 TITLE OF INVENTION: Interacting Proteins
 FILE REFERENCE: 15966-523
 CURRENT APPLICATION NUMBER: US/09/266,225D
 CURRENT FILING DATE: 1999-03-10
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 12
 LENGTH: 816
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-266-225D-12

Alignment Scores:
 Pred. No.: 1.63e-10 Length: 816
 Score: 244.50 Matches: 170
 Percent Similarity: 34.47% Conservative: 82
 Best Local Similarity: 23.26% Mismatches: 252
 Query Match: 6.03% Indels: 227
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US-09-836-392-8_COPY_22_2205 (1-2184) x US-09-266-225D-12 (1-816)

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700 AAGAGCCCGACTTTTCCACCTTCATGT-----
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351 HisAspProAspAsp-GluProAspCysAlaProProPheAspPheAlaPheAspArgGl 370
728 -----ATGAACTGTCTCTG-----
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743 -----GGAAGCAGAG-----CAGCCTTCTTCTCATCCCGAGGCCAG 777
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778 GAGTACACCGTGGTGTGGTGGTAAAGAGAGGAGTCCAGAACTACACGGTGGTGNAC 837
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422 -----
838 ACAGAGAAGGCCCTCATGTGAGGTGCAGAGAGTGTGCTGCCCTGGGATGAAGTGCAGTGC 897
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955 TACACCTCAAGGGCATGCCCTTAAACACACCCACAGCGCTTGGATATCCAGCT 1014
453 uGlnProProProValSerGluProAlaProProIleGlyAspGlyAlaIleSerAs 473
1015 GTGCTACCTGCTTCTTGGCGGCTGTATTAAAGAAATTCCTAGTCTTACGC 1074
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GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

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Prad. No. is the number of results predicted by chance to have a
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ALIGNMENTS

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; Patent No. US20020173458A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptides,
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: PTO20P1
; CURRENT APPLICATION NUMBER: US/09/836,392
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: PCT/US00/28066
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 60/159,542
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/165,914
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/189,027
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 728
; TYPE: PRT

ORGANISM: Homo sapiens

J9-836-392-21

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TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROIDS
FILE REFERENCE: SCH-1811
CURRENT APPLICATION NUMBER: US/10/132,382
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 1987
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ORGANISM: Homo sapiens
0-132-382-6

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1861 SerAspArgSerGluHisAspLeuThrProMetAspGlyGluThrPheSerGlnHisLeu 1880
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1901 ValIleValIleGlyLeuGluIlysAspSerGlyAlaGlnArgGlyArgValIleAlaVal 1920
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1981 TTAAAAGCCCGAGAGCTGACTCCGCATCGGGTGCTGTGGATGCTGCCGTGGTGGCAAAG 2040
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1941 AspThrValValCysThrPheGluAsnGlnAsnThrGluTrpCysLeuAlaValTrpArg 1960
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1961 GlyTrpGlyAlaArgGluPheAspIlePheTyrGlnSerTyrGluGluLeuGlyArgLeu 1980
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2161 GAGCGTTGCACTCCACAGACA 2181
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1981 GluAlaCysThrArgLysArg 1987

3

10-132-382-2

sequence 2, Application US/10132382

Publication No. US20
GENERAL INFORMATION:

APPLICANT: WEISS, BERTRAM

TITLE OF INVENTION: MEMBRANE

FILE REFERENCE: SCH-1811
CURRENT APPLICATION NUMBER

CURRENT FILING DATE: 2002-04-26

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PATENTIN ver. 2.1
EO ID NO 2

LENGTH: 20

TYPE: PRT

ORGANISM:
10-132-382-

[illegible]

gment Score

re:
T. No.:

cent Similarity: 94.50% Conservative: 0

t Local Similarity:	94.50%
Mismatches:	1

LY MATCH:	88.09%	INDERS:	33
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09-836-392-8 COPY 22 2205 (1-2184) X US-10-132-382-2 (1-2013)

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Db	1346	AlaSerMetLeuHis	AlaLeuGlnHisProCys	IleValAlaLeu	IleSerIle	1365
QY	121	CACCGCTCTGCT	TGCGCTGTGAGCTGCGGCGCTCAG	CGCTCAACACCGTGTCTGCTCC		180
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QY	241	TACCAGATCGCCT	CGGCGCTGCGCTACCTGCACAGAAAA	CAATCATCTTCTGTGACCTG		300
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Db	1506	HisGlnLeuGlnIle	AlaLysLysLeuSerLysGlyIleArg	ProValLeuGlyGlnPro		1525
QY	601	GAGGAAGTGCAG	TTCGGCGACTGCAGGCGCTCATGATG	GTGTGGGACACTAAGCCA		660
Db	1526	GluGluValGlnPhe	ArgArgLeuGlnAlaLeuMetMetGluCys	TrpAspThrLysPro		1545
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2161 GAGGCTTGCACTCGCAAGAGA 2181

Db 2007 GluAlaCysThrArgLysArg 2013
RESULT 4
US-10-132-382-8
; Sequence 8, Application US/10132382
; Publication No. US20030045699A1
; GENERAL INFORMATION:
; APPLICANT: WEISS, BERTRAM
; TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROLS
; FILE REFERENCE: SCH-1811
; CURRENT APPLICATION NUMBER: US/10/132.382
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 2014
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-382-8
Alignment Scores:
Pred. No.: 4,98e-215 Length: 2014
Score: 3574.50 Matches: 687
Percent Similarity: 94.50% Conservative: 0
Best Local Similarity: 94.50% Mismatches: 1
Query Match: 88.09% Indels: 39
DB: 15 Gaps: 1
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RESULT 5
US-10-132-382-4
; Sequence 4, Application US/10132382
; Publication No. US20030045699A1
; GENERAL INFORMATION:
; APPLICANT: WEISS, BERTRAM
; TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROLS
; FILE REFERENCE: SCH-1811
; CURRENT APPLICATION NUMBER: US/10/132,382
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2040
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-382-4

Alignment Scores:
Pred. No.: 4,99e-215 Length: 2040
Score: 3574.50 Matches: 687
Percent Similarity: 94.50% Conservative: 0
Best Local Similarity: 94.50% Mismatches: 1
Query Match: 88.09% Indels: 39
DB: 15 Gaps: 1

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 1621 ATCTGATCCACAGGAATCACTCACTGACTACTGTCTCCATGTCTCTCTCTCTCTCTCTCC 1680
 1854 IleLeuIleHisGlnGlnSerLeuThrAspTyrCysSerMetSerSerTyrSerSerSer 1873
 1581 CCACCCCGCAGCTGCCAGTCCCTCAAGCCTCCCGAGCTCCCGCAGCAAGTCTCTCC 1740
 1874 ProProGlnAlaAlaArgSerProSerSerLeuProSerSerProAlaSerSerSer 1893
 1741 AGTGTGCTTTCTCCACCGACTCGGAGGACTCAGACATCTATACATACGCGCGGTGAGAT 1800
 1894 SerValProPheSerThrAspCysGluAspSerAspMetLeuHisThrProGlyAlaAla 1913
 1801 TCGACAGTCTCAGACATGACCTGACCCCGATGGAGCGGAGACCTTCAGCCAGCACCTG 1860
 1914 SerAspArgSerGluHisAspLeuThrProMetAspGlyGluThrPheSerGlnHisLeu 1933
 1861 CAGCCCTGAAGATCTCGCGCTCAGAGACCTCATTTGGTCCCGAGCGCGGTGGAGAT 1920
 1934 GlnAlaValLysIleLeuAlaValArgAspLeuIleTrpValProArgArgGlyGlyAsp 1953
 1921 GTTATCTCTATTGGCTGGAGAAGATTCTGAAGCCACCGCGGCGCGAGTCAATTCGCGTC 1980
 1954 ValIleValIleGlyLeuGluLysAspSerGlyAlaGlnArgGlyArgValIleAlaVal 1973
 1981 TTAAGCCCGAGAGTGTCTCCGATGGGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040
 1974 LeuLysAlaArgGluLeuThrProHisGlyValLeuValAspAlaValValAlaLys 1993
 2041 GACACTTGTGTGCACCTTTGAAATGAAACACAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2100
 1994 AspThrValValCysThrPheGluAsnGluAsnThrGluTrpCysLeuAlaValTrpArg 2013
 2101 GGCTGGCGCGCGAGGAGTTCGACATTTCTACAGTCTCTACGAGAGTGTGTGTGTGTGTGTGTGT 2160
 2014 GlyTrpGlyAlaArgGluPheAspIlePheTyrGlnSerTyrGlnLeuGlyArgLeu 2033
 2161 GAGGCTTGCCTCGCAAGAGA 2181
 2034 GluAlaCysThrArgLysArg 2040

RESULT 6

US-10-094-749-1689
 ; Sequence 1689, Application US/10094749
 ; Publication No. US20030219741A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ISOGAI, TAKAO
 ; APPLICANT: SUGIYAMA, TOMOYASU
 ; APPLICANT: OTSUKI, TETSUJI
 ; APPLICANT: WAKAMATSU, AI
 ; APPLICANT: SATO, HIROYUKI
 ; APPLICANT: ISHII, SHIZUKO

APPLICANT: YAMAMOTO, JUN-ICHI

APPLICANT: ISONO, YUUKO

APPLICANT: HIO, YURI

APPLICANT: OTSUKA, KAORU

APPLICANT: NAGAI, KEIICHI

APPLICANT: IRIE, RYOTARO

APPLICANT: TAMECHIKI, ICHIRO

APPLICANT: SEKI, NAOHIKO

APPLICANT: YOSHIKAWA, TSUTOMU

APPLICANT: OTSUKA, MOTOKYUKI

APPLICANT: NAGAHARI, KENJI

APPLICANT: MASUHO, YASUHIKO

TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA

FILE REFERENCE: 084335/0160

CURRENT APPLICATION NUMBER: US/10/094,749

PRIORITY FILING DATE: 2002-03-12

PRIOR APPLICATION NUMBER: 60/350,435

PRIOR FILING DATE: 2002-01-24

PRIOR FILING DATE: 2001-09-14

NUMBER OF SEQ ID NOS: 3381

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1689

LENGTH: 501

TYPE: PRT

ORGANISM: Homo sapiens

10-094-749-1689

Invent Scores:

i. No.: 1,05e-155 Length: 501

Matches: 501

Conservative: 0

Mismatch: 0

Indels: 1

Gaps: 0

09-836-392-8_COPY_22_2205 (1-2184) x US-10-094-749-1689 (1-501)

478 ATGTTCTCTATGGAATGCTCTACGAGTTGCTGTCAGGACGCGCTGCACTGGGC 537

1 Met:PheSerTyrGlyMetValLeuTyrGluLeuLeuSerGlyGlnArgProAlaLeuGly 20

538 CACCACAGCTCCAGATGTCACAAAGAGCTGTCCAGGGCATCCGCCGGTCTCTGGGGCAG 597

21 HisGlnLeuGlnIleAlaLysLeuSerLysGlyLeuArgProValLeuGlyGln 40

598 CCGGAGAAAGTGCAGTTCCGCGACTGCGAGGGCTCATGATGAGTGTGGGACACTAAG 657

41 ProGluGluValGlnPheArgArgLeuGlnAlaLeuMetMetGluCysTrpAspThrLys 60

658 CCAGAGAAGCGACCGCTGGCCCTGTCGGTGGTGAGCCAGATGAAGGACCCGACTTTTGGC 717

61 ProGluLysArgProLeuAlaLeuSerValSerGlnMetLysAspProThrPheAla 80

718 ACCTTCATGATGAGTGTGCTGTGGAGAGCAGACAGAGCTTCTTCTCATCCAGGGCCAG 777

81 ThrPheMetTyrGluLeuLysCysGlyLysGlnThrAlaPheSerSerGlnGlyGln 100

778 GAGTACACCGTGTGTTTGGGATGGAAGAGAGAGTCCAGAACTACACGGTGTGAAC 837

101 GluTyrThrValValPheTrpAspGlyLysGluLysLeuSerArgAsnTyrThrValValAsn 120

838 ACAGAGAAGGCGCTCATGGAGTGCAGAGGATGTGTCCTCGGGATGAAGTGTGAGTGC 897

121 ThrGluLysGlyLeuMetGluValGlnArgMetCysCysProGlyMetLysValSerCys 140

898 CAGTCCAGGTCAGAGATCCCTGTCAGACAGCCAGCCAGGACAGAAATCTACATCTAC 957

141 GlnLeuGlnValGlnArgSerLeuTrpThrAlaThrGluAspGlnLysIleTyr 160

958 ACCCTCAAGGCGCATGTGCCCCCTTAAACACACACCCCAAGCGCTTGGATCTCCAGCTGTC 1017

161 ThrLeuLysGlyMetCysProLeuAsnThrProGlnGlnAlaLeuAspThrProAlaVal 180

1018 GTCACCTGCTTCTTGGCGCTGCTGTTATTATAAAGAATTCTTACCTGCTTTCAGCGGC 1077

181 ValThrCysPheLeuAlaValProValIleLysLysAsnSerTyrLeuValLeuAlaGly 200

1078 CTCGCCGATGGCTTGTGGTGTGTTTCCCGTGGTGGGGGACCCCAAGGACAGCTGC 1137

201 LeuAlaAspGlyLeuValAlaValPheProValValArgGlyThrProLysAspSerCys 220

1138 TCCTACCTGTGCTCACACAGCCACAGTCCAAAGTTCAGATTCGCGGATGAAGACGCA 1197

221 SerTyrLeuCysSerHisThrAlaAsnArgSerLysPheSerIleAlaAspGluAspAla 240

1198 CGGCGAAGCCCTACCCAGTCAAGCCATGAGGTGCTCAACAGCGCTCTGAGGTCTGG 1257

241 ArgGlnAsnProTyrProValLysAlaMetGluValValAsnSerGlySerGluValTrp 260

1258 TACAGCAATGGCGCGGCTCTTGTCTCATGCTGCTGCTCTCTCTCTCTCTCTCTCTCT 1317

261 TyrSerAsnGlyProGlyLeuLeuValIleAspCysAlaSerLeuGluIleCysArgArg 280

1318 CTGGAGCCCTACATGGCCCTCTCATGTTACGTACGTGCTGCTGCTGCTGCTGCTGCTG 1377

281 LeuGluProTyrMetAlaProSerMetValThrSerValValCysSerSerGluGlyArg 300

1378 GGGGAGGAGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1437

301 GlyGluGluValValTrpCysLeuAspAspLysAlaAsnSerLeuValMetTyrHisSer 320

1438 ACCACCTACGAGTGTGTGCGCGTACTTCTGCGGGTCTCCAGCCCTCAGGACATG 1497

321 ThrThrTyrGlnLeuCysAlaArgTyrPheCysGlyValProSerProLeuArgAspMet 340

1498 TTTCCCGTGGCGCTTGGACACGGAACCCCGGCGAGCCAGCCACAGGCGCAACCCAAAG 1557

341 PheProValArgProLeuAspThrGluProAlaAlaSerHisThrAlaAsnProLys 360

1558 GTGCTGAGGGGAGTCCATCCGCGAGCTGAGCATGATGATGATGATGATGATGATGATG 1617

361 ValProGluGlyAspSerIleAlaAspValSerIleMetTyrSerGluGluLeuGlyThr 380

1618 CAGATCCTGATCCACCGAATCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 1677

381 GlnIleLeuIleHisGlnGlnSerLeuThrAspTyrCysSerMetSerTyrSerSer 400

1678 TCCCAACCCCGCGAGCTGCCAGGTCCCTCCCTCAAGCTCCCGAGTCCCGAGCAAGTCT 1737

401 SerProProArgGlnAlaAlaArgSerProSerSerLeuProSerProAlaSerSer 420

1738 TCAGTGTGCTTCTTCCACCGAGTCCGAGGACTCAGACATGCTACATCGCCCGGTGCT 1797

421 SerSerValProPheSerThrAspCysGluAspSerAspMetLeuHisThrProGlyAla 440

1798 GCTCCGACAGGTCTGAGCATGACCTGACCCCTGAGACGGGAGAGCTTCAGCCAGCAC 1857

441 AlaSerAspArgSerGluHisAspLeuThrProMetAspGlyGluThrPheSerGlnHis 460

1858 CTGACGCGCTGAAAGATCTCCCTGAGACCTCATTTGGTCCCGAGCGCGGTGGA 1917

461 LeuGlnAlaValIleLeuAlaValArgAspLeuIleTrpValProArgArg-ValGln 480

1918 GATGTTTATCGTTCATTTGGCTGAGAGGATTCGAAAGCCAGCGGGCGGAGTCATTGCC 1977

480 uMetLeuSerSerLeuAlaTrpArgArgIleLeuLysProSerGlyAlaGluSerLeuP 500

1978 GTCT 1981

500 oSer 501

RESULT 7

US-10-143-133-2

; Sequence 2, Application US/1043133

; Publication No. US20020197658A1

NEPAL INFORMATION:
 APPLICANT: Yoganathan, Thillainathan
 APPLICANT: Delaney, Allen
 TITLE OF INVENTION: Cancer Associated Protein Kinase and Its Use
 TITLE REFERENCE: KINE-023
 CURRENT APPLICATION NUMBER: US/10/143,133
 PRIORITY FILING DATE: 2002-05-09
 PRIOR APPLICATION NUMBER: 60/290,555
 PRIOR FILING DATE: 2001-05-10
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSeq for Windows Version 4.0
 Q. ID NO. 2
 LENGTH: 847
 TYPE: PRT
 ORGANISM: Homo sapien
 0-143-133-2

Alignment Scores:
 L. No.: 5,56e-13 Length: 847
 e: 337.50 Matches: 195
 ent Similarity: 34.09% Conservative: 75
 Local Similarity: 24.62% Mismatches: 241
 y Match: 8.32% Indels: 283
 14 Gaps: 38

9-836-392-8_COPY_22_2205 (1-2184) x US-10-143-133-2 (1-847)

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52 CGCGAGGAGGCGCAGCATGTCAGCCGCTGCAGACCCCTGCATCTGTGGCGCTCATCGGC 111
162 ArgGlnGluAlaArgLeuPheAlaMetLeuAlaHisProAsnIleAlaLeuLysAla 181
112 ATCAGCATCCACCCG-----CTCGCTTCGCCCTGGAGCTCGCGCGCTCAGCAGCCTC 165
182 ValCysLeuGluGluProAsnLeuCysLeuValMetGluTyrAlaAlaGlyGlyProLeu 201
166 AACACCGTCTCTCCGAGAACCCAGAGATTCTTCCTTTATACCCCTGGGACATGCTC 225
202 SerAlaLeuAlaGlyArgArg-----ValPro-----ProHisValLeu 215
226 ACCCAAAATAAGCTACAGATCCCTCGCGCTGGCGCTGACCTGCACCAAGAA----- 279
216 Val-----AsnTrpAlaValGlnIleAlaArgGlyMetHisTyrLeuHisCysGluAlaLeu 234
280 ---AACATCATCTTCTGTGACCTGAAGTCGGACACACATCTCTGTGTGG-----TCC 327
235 ValProValIleHisArgAspLeuLysSerAsnAsnIleLeuLeuLeuGlnProIleGlu 254
328 CTTCAGCTCAGGACACATCAACATCAAGCTATCTGACTACGGGATTTGAGGACGTCA 387
255 SerAspMetGluHisLysThrLeuLysIleThrAspPheGlyLeuAlaArgGluTrp 274
388 TTCCATGAGGGCGCCTAGGCGCTGGAGGCGCACTCTCGCTACCAAGCCCGCAGAGATCAGG 447
275 HisLysThrThrGlnMetSerAlaAlaGlyThrTyrAlaTrpMetAlaProGluValIle 294
448 CTTCGATTTATATGATGAGAGGTAGATGTTCTCTCTATGAAATGGTGCTCTACGAG 507
295 LysAlaSerThrPheSerLysGlySerAspValTrpSerPheGlyValLeuLeuTrpGlu 314
508 TTGCTGTACGACGACGGCCCTGCACTCGTGGCCACCCAGCAGCTCCAGATTGCG----- 558
315 LeuLeuThrGlyGluValProTyrArgGlyIleAspCysLeuAlaValAlaTyrGlyVal 334
559 -----AAGAGCTGTCCAAAGGCGATCCGCCGCTTCTGGGCGAGCCGAGGAGTGCAG 612
335 AlaValAsnLysLeuThrLeuProIleProSerThrCysProGluPro----- 350
613 TTCCGGCGACTCAGCGCTCATGATGATGAGTCTGGACACTTAAGCCAGAGACGACCG 672
351 -----PheAlaGlnLeuMetAlaAspCysTrpAlaGlnAspProHisArgArg--- 366
673 CTGGCCCTCTCGTGTGAGCAGCATGAAGACCCGACCTTTTGGCACCTTCATGATGAA 732
  
```

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367 -----ProAspPheAlaSerIleLeuGlnGln 375
733 CTGTG-CTGTGGGAAGCAGACAGACCTTCTTCTCATCCAGGCGCAGAGTACACCGTGGT 791
376 LeuGluAlaLeuGluAlaGlnValLeuArgGluMetProArgAspSerPheHisSerMet 395
792 GTTTTGGGATGGAAAAGAGGAGTCCAG----- 818
396 GlnGluGlyTrpLysArgGluIleGlnGlyLeuPheAspGluLeuArgAlaLysGluLys 415
818 ----- 818
416 GluLeuLeuSerArgGluGluGluLeuThrArgAlaAlaArgGluGlnArgSerGlnAla 435
819 ---GAACCTACACCGTGTGTGAAC- 839
436 GluGlnLeuArgArgGluHisLeuLeuAlaGlnTrpGluLeuGluValPheGluArg 455
840 -----AGAGAAGGCGCTCAT----- 854
456 GluLeuThrLeuLeuLeuGlnGlnValAspArgGluArgProHisValArgArgArgArg 475
855 -----GGAGTGCACAGGATGTGTCGCC 878
476 GlyThrPheLysArgSerLysLeuAlaArgAspGlyGlyGluArgIleSerMetPro 495
879 TGGATGAGTGAGCTG----- 896
496 LeuAspPheLysHisArgIleThrValGlnAlaSerProGlyLeuAspArgArgArgAsn 515
897 -----CCAGCTCCAGGTCACAGATCCCTGT----- 922
516 ValPheGluValGlyProGlyAspSerProThrPheProArgPheArgAlaIleGlnLeu 535
923 -----GACAG-----CCACGAGGACCAGAAATCT 949
536 GluProAlaGluProGlyGlnAlaTrpGlyArgGlnSerProArgArgLeuGluAspSer 555
950 ACATCTACACCTCAAGGCGATGTGCCCTTAAACACACCCCAACAGGCTTGGATACTC 1009
556 SerAsnGlyGluArgArgAlaCys-----TrpAlaTrp 566
1010 CAGCTGTGTCACCTGTCTTCTGGCGCTGCTGTATTAAAGA----- 1054
567 GlyProSerProLysProGlyGluAlaGlnAsnGlyArgArgSerArgMetAsp 586
1055 ATTCTACCTGG-----TCTTACGGCGCTCCCGAGTGGCTGTGGCTGTGTTTC 1105
587 GluAlaThrTrpTyrLeuAspSerAspSerProLeuGlySerProSerThrPro 606
1106 CCGTGTGTGC---GGGCGACCCCAAGGACAGCTGCTCTACCTGTGCTCACACACGCCA 1162
607 ProAlaLeuAsnGlyAsnProProArg-----ProSerLeuGluProGluGluPro 623
1163 ACAGTCCAGTTCAGCATCGCGATCAAGCAGCGGACAGACCCCTACCCAGTGAAG 1222
624 LysArgProValProAlaGluArgGlySerSerGly---ThrPro----- 638
1223 CCATGGAGGTGGTCAACAGCGGCTCTGAGTCTGGTACAGCAATGGCGCGGCTCTCTG 1282
639 -----LysLeuIleGlnArgAlaLeuLeuArgGlyThrAlaLeu---LeuAlaSerLeu 655
1283 -----TCATCG 1288
656 GlyLeuGlyArgAspLeuGlnProProGlyGlyProGlyArgGluArgGlyGluSerPro 675
1289 ACTGTGCTCTCCAGATCTCGAGGCGGTGAGCGCTTACATGGCCCCCTCCATGGTTA 1348
676 ThrThrProProThrProThrProAlaPro---CysProThrGluProProPro---Ser 693
1349 CGTGAGTGTGTGAGTCTGAGGCGCAG- 1378
694 ProLeuIleCysPheSerLeuLysThrProAspSerProProThrProAlaProLeuLeu 713
  
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1379 -----GGAGGAGGTCCTGCTGGTGCCTGGATGACAGGCCACT 1417
1380 |||:|||||:
714 LeuAspLeuGlyIleProValGlyInArgSerAlaLysSerProArgArgGluGluGlu 733
1418 CTTTGGTGTATGATACCACTCCACCACTACCACTGCTGTGCGCGGTACTTCTGCGGGTCC 1477
1419 |||:|||||:
734 ProArgGlyGlyThrValSerProPro-----ProGlyThrSerArgSerAla 749
1478 CCAGCCCTCAGGACATGTTCCGCTGCGCGCTTGGACACGGAACCCCGGACGCCA 1537
1479 |||:|||||:
750 ProGlyThrProGlyThr-----ProArgSerPro 759
1538 -----GCCACAGGCGCAACCAAGGTGCTGAGGGGACTCCATCGCGAGC 1585
1539 |||:|||||:
760 ProLeuGlyLeuIleSerArgPro-----ArgProSerProLeuArgSer 774
1586 TGAGCATCATGTACAGTAGAGAGCTGGGCGACGACATCTGATCCACCAAGATCACTCA 1645
1587 |||:|||||:
775 -----ArgIleAspProTrp-----Ser 780
1646 CTGACTACTGCTCCATGCTCTCTACTCTCATCCACCCGCGCAGGCTGCCAGGTCCC 1705
1647 |||:|||||:
781 PheValSerAla-----GlyProArgProSerProLeuProSerPro 794
1706 CTTCAAGCTCCCGAGTCCCGACGAAGTTCTTCCAGTGTCCCTTCTCCACGACTGG 1765
1707 |||:|||||:
795 -----GlnProAlaProArgAla---ProTrpThrLeuPheProAspSerAsp 810
1766 AGGACTCAGACATGTACATACGCCCGGTGCTGCTCCGACAGGTCTGAGCATGACCTGA 1825
810 ----- 810
1826 CCCCCATGACGGGAGACCT---TCAGCAGACCTGCAGCGCGTGAAGATCTCGCG 1882
811 ProPheTrpAspSerProProAlaasn-ProPheGlnGlyProGlnAspCysArgAl 830
1883 TCAGACACTCATTTGGTCCCGAGCGCGGTGG 1916
830 aGlnThrLysAspMetGlyAlaGlnAlaProTrp 841
JLT 8
10-115-482-48
sequence 48, Application US/10115482
Application No. US20030212257A1
GENERAL INFORMATION:
APPLICANT: Spytek, et al.
TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM
TITLE OF INVENTION: AND METHODS
TITLE OF INVENTION: OF USING THE SAME
FILE REFERENCE: 21404-322D
CURRENT APPLICATION NUMBER: US/10/115,482
CURRENT FILING DATE: 2002-04-05
PRIORITY APPLICATION NUMBER: 60/281,086
PRIORITY FILING DATE: 2001-04-03
PRIORITY APPLICATION NUMBER: 60/281,136
PRIORITY FILING DATE: 2001-04-03
PRIORITY APPLICATION NUMBER: 60/281,863
PRIORITY FILING DATE: 2001-04-05
PRIORITY APPLICATION NUMBER: 60/281,906
PRIORITY FILING DATE: 2001-04-05
PRIORITY APPLICATION NUMBER: 60/282,934
PRIORITY FILING DATE: 2001-04-10
PRIORITY APPLICATION NUMBER: 60/283,512
PRIORITY FILING DATE: 2001-04-12
PRIORITY APPLICATION NUMBER: 60/285,325
PRIORITY FILING DATE: 2001-04-19
PRIORITY APPLICATION NUMBER: 60/285,890
PRIORITY FILING DATE: 2001-04-23
PRIORITY APPLICATION NUMBER: 60/286,068
PRIORITY FILING DATE: 2001-04-24
PRIORITY APPLICATION NUMBER: 60/286,292
PRIORITY FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/287,213
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 60/288,257
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/291,134
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/282,020
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/291,725
PRIOR FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 60/294,771
PRIOR FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 60/296,965
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: 60/299,128
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 149
SEQ ID NO 48
LENGTH: 915
TYPE: PRT
ORGANISM: Homo sapiens
US-10-115-482-48
Alignment Scores:
Pred. No.: 7,49e-13 Length: 915
Score: 335.50 Matches: 106
Percent Similarity: 46.19% Conservative: 76
Best Local Similarity: 26.90% Mismatches: 159
Query Match: 8.27% Indels: 53
DB: 12 Gaps: 14
US-09-836-392-8_COPY_22_2205 (1-2184) x US-10-115-482-48 (1-915)
QY 28 GCCATGAGAACTTCTCCGAG-----TTCCGCGAGGAGGCCAGCATG 69
DB 298 AlaValLysIlePheAenLysHisThrSerLeuArgLeuLeuArgGlnLeuValVal 317
QY 70 CTGCACGCGCTGCAGCAGCCCTGTCATCGTGGCGCTCATCGGCATCAGCATCCACCGCTC 129
DB 318 LeuCysHisLeuHisHisProSerLeuIleSerLeuLeuAlaAlaGlyIleArgProArg 337
QY 130 TCGTTCGCGCTGGAGCTCGCGCCCTCAGCAGCTCAACACCGCTGTGTCGAGAGACGCC 189
DB 338 MetLeuValMetGluLeuAlaSerLysGlySerLeuAspArgLeuGlnGlnAspLys 357
QY 190 AGAGATTCTCTCTTATACCCCTGGGACACATGCTCAACCAAAATAGCTTACCAGATC 249
DB 358 AlaSer-----LeuThrArgThrLeuGlnHisArgIleAlaLeuHisVal 372
QY 250 GCTCGGCGCTGGCTACCTGCACAGAAACATCATCTTCTGTGACCTGAAGTCGGAC 309
DB 373 AlaAspGlyLeuArgTyLeuHisSerAlaMetIleIleTyArgAspLeuLysProHis 392
QY 310 AACATTCTGGTGTGCTCCCTTGACGTCAAGGAGCACATCAACATCAAGCTATCTGACTAC 369
DB 393 AenValLeuLeuPheThrLeuTyProAsnAlaAlaIleAlaLysIleAlaAspTy 412
QY 370 GGGATTTCAGCAGCTCATTCATGACGGCGCCCTTAGCGGTGGAGGCGCATCTCTGGTAC 429
DB 413 GlyIleAlaGlnTyCysCysArgMetGlyIleLysThrSerGluGlyThrProGlyPhe 432
QY 430 CAGGCCCCAGAGATC---AGGCTCGCATTTATATGATGAGAGGTAGATATGTTCTCC 486
DB 433 ArgAlaProGluValAlaArgGlyAsnValIleTyArgGlnGlnAlaAspValTySer 452
QY 487 TATGAATGGTCTCTACGAGTTGCTG---TCAGACAGCGCCCTGCACCTGGGC----- 537
DB 453 PheGlyLeuLeuLeuTyArgAspIleLeuThrThrGlyGlyArgIleValGluGlyLeuLys 472
QY 538 -----CACACAGCTCCAGATTGCCAAGAGCTGTCCAAGGGATCCGCCCG 585
DB 473 PheProAsnGluPheAspGluLeuGlnGlyLysLeuProAspProValLysGlu 492
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1084 GATGGCTTGTGGCTGTGTTT 1104
||||| :|||:|||||
1566 AspGlyLeuAlaIlePhe 1572

LIT 11
10-335-687A-5
sequence 5, Application US/10335687A
Application No. US20030166222A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
TITLE OF INVENTION: 39267, Human Kinase Family Members and
APPLICANT: Meyers, Rachel E.
TITLE OF INVENTION: Uses Therefor
FILE REFERENCE: MPI02-001PRNM
CURRENT APPLICATION NUMBER: US/10/335,687A
CURRENT FILING DATE: 2003-01-02
PRIORITY APPLICATION NUMBER: 60/345,773
PRIORITY FILING DATE: 2002-01-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1824
TYPE: PRT
ORGANISM: Homo sapiens
10-335-687A-5

Alignment Scores:
I. No.: 2,6e-12 Length: 1824
e: 327.50 Matches: 101
ent Similarity: 45.48% Conservative: 75
Local Similarity: 26.10% Mismatches: 168
Y Match: 8.07% Indels: 43
12 Gaps: 13

19-836-392-8_COPY_22_2205 (1-2184) x US-10-335-687A-5 (1-1824)
28 GCATGAAGAACTTCTCCGAG-----TTCCGGCAGGAGCCGACGATG 69
||||| :|||:|||||
1201 AlaValLysPheAsnLysHisThrSerLeuArgLeuLeuArgGlnGluLeuValVal 1220
70 CTGACGCGCTCAGACACCCCTGCGATCGTGGGCTCATCGGCATCAGCATCCACCGCTC 129
||||| :|||:|||||
1221 LeuCysHisLeuHisProSerLeuLeuSerLeuLeuAlaAlaGlyIleArgProArg 1240
130 TGCTTCGCTGAGCTCGCGCTCAGACGCTCAGACGCTCAGACGCTGCTCGGAGACGCC 189
||||| :|||:|||||
1241 MetLeuValMetGluLeuAlaSerLysGlySerLeuAspArgLeuLeuGlnGlnAspLys 1260
190 AGAGATTCTTCTTTATACCCCTGGGACACATGCTCACCCAAAAAATAGCTACCATC 249
||||| :|||:|||||
1261 AlaSer-----LeuThrArgThrLeuGlnHisArgIleAlaLeuHisVal 1275
250 GCTCGGCGCTGCTTACCTGCACAGAAACATCATCTTCTGTGACCTGAGTGGAC 309
||||| :|||:|||||
1276 AlaAspGlyLeuArgTyLeuHisSerAlaMetIleIleTyArgAspLeuLysProHis 1295
310 AACATTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 369
||||| :|||:|||||
1296 AsnValLeuLeuPheThrLeuTyProAsnAlaAlaIleAlaLysIleAlaAspTy 1315
370 GGGATTTCAGGCGAGTATTCATCCAGGCGCCCTAGCGGTGGAGGCGACTCTCGGTAC 429
||||| :|||:|||||
1316 GlyIleAlaGlnTyCysCysArgMetGlyIleLysThrSerGluGlyThrProGlyPhe 1335
430 CAGGCCCCAGAGATC---AGGCTCGCATTTATATGATGAGAGGTAGATGTTCTTCC 486
||||| :|||:|||||
1336 ArgAlaProGluValAlaArgGlyAsnValIleTyAsnGlnGlnAlaAspValTySer 1355
487 TATGGAATGGTCTTACGAGTTGCTG---TCAGACAGCGCCCTGCACTGGCG--- 537
||||| :|||:|||||
1356 PheGlyLeuLeuLeuTyAspIleLeuThrThrGlyGlyArgIleValGluGlyLeuLys 1375

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362	Db	AlaMetAsnLysLeuAlaLeuProfilProSerThrCysProGluPro-----	377
613	QY	TTCCGGCGACTGCAGGCGCTTCATGATGGAGTCTGGGACACTAAGCGACAGAAGCGACCG	672
378	Db	-----PheAlaLysLeuMetGluAspCysTrpAsnProAspProHisSerArg--	393
673	QY	CTGGCCCTGTGGTGTGGACCCAGATGAAGGACCGACTTTTGGCCACCTTCATCATGAA	732
394	Db	-----ProSerPheThrAsnLeuLeuAspGln	402
733	QY	CTGTGCTGTGGGAAGCAGACAGCCTTCTTCTC-ATCCAGCGCCAGGATACACCGTGT	791
403	Db	LeuThrThrIleGluGluSerGlyPhePheGluMetProLysAspSerPheHisCysLeu	422
792	QY	TTTTTGGGATGGAAAAGAGAGGTCAGGAACCTACACGGT-----GGTGAACACAGA	842
423	Db	GlnAspAsnTrpLysHisGluIleGlnGluMetPheAspGlnLeuArgAlaLysGluLys	442
843	QY	GAA-----GGGCTCATGGAGGTGCAGAG	866
443	Db	GluLeuArgThrTrpGluGluGluLeuThrArgAlaAlaLeuGlnGlnLysAsnGlnGlu	462
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522	Db	erAspPheGlnHisLysPheThrValGlnAlaSerProThrMetAspLysArgLysSerL	542
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542	Db	eulleAsnSerArgSerSerProAlaSerProThrIleIleProArgLeuArgAlaI	562
1045	QY	-----	1045
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1046	QY	-----TTAAAAGAATTCCT-----ACCTGGCTTAGC	1073
582	Db	luGluGlyGluGluGluLysArgAlaProLysLysGlyArgThrTrpGly-Pro	601
1074	QY	GGGCT-----	1079
602	Db	glyThrLeuGlyGlnLysGluLeuAlaSerGlyAspGluGlyLeuLysSerLeuValAsp	621
1080	QY	-----CGCCGATGGCTTGTGCTGTGTTCCGTGTGCGGGCACCCCAAGGACAG	1133
622	Db	glyTyrLysGlnTrpSerSerSerAlaProAsnLeuValLysGly--ProArgSerSer	640
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1194	QY	CGCAGCGAGAACCCCTTACCAGTGAAGGCCATGAGGTGTCAACACGGCTCTGAGGT	1253
653	Db	-----GluAspGluAspSerGluGlyProGlySerGlyGluSerArgLeu-----	667
1254	QY	CTGGTACAGCAATGGGCGGGCTCTCTGTGTCAGCTGTGCTCCCT-----	1301
668	Db	-----GlnHisSerProSerGlnSerTyrLeuCysIleProPheProArgGly	683
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704 AlaThrSerThrProGlnLeuThrProThrAsnSerLeuLysArgGlyGlyAla----- 721
1395 GTCCCTGGATGACAGGCCAACCTCTTGTGTGTATGATACCACTCCACCACTACCACTGTG 1454
722 -----HisHis-----ArgArg 725
1455 TGCCCGTACTTCTCGGGGT----- 1475
726 CysGluValAlaLeuLeuGlyCysGlyAlaValLeuAlaAlaThrGlyLeuGlyPheAsp 745
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922 lSerSerSerPheLeuPheProPhePheValProGlnGlyMetLeuLysThrP 942
1977 CGTCT 1981
942 rSer 943

LT 13
0-153-668-438
quence 438, Application US/10153668
blication No. US20030092616A1
GENERAL INFORMATION:
APPLICANT: HONDA, Goichi
APPLICANT: MATSUDA, Akio
APPLICANT: MURAMATSU, Shuji
APPLICANT: ISHIZAWA, Kenya
TITLE OF INVENTION: STAT6 Activating Gene
FILE REFERENCE: 1254-0207P

CURRENT APPLICATION NUMBER: US/10/153,668
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 60/293,172
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/316,031
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/328,403
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: JP 2001-157043
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: JP 2001-260681
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: JP 2001-313175
NUMBER OF SEQ ID NOS: 488
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 438
LENGTH: 892
TYPE: PRT
ORGANISM: Homo sapiens
US-10-153-668-438

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Pred. No.: 1,76e-10 Length: 892
Score: 297.50 Matches: 168
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Best Local Similarity: 22.40% Mismatches: 256
Query Match: 7.33% Indels: 236
DB: 15 Gaps: 31

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QY 85 CACCCCTCATCTGTGGCGCTCATCGCATCAGCATCCCGCTCTCTCTCGCC----- 138
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QY 139 CTGGAGCTCGCGCGCTCAGCAGCTCAACACCGTGTCTCCGAGAACGCCAGAGATTCT 198
DB 223 MetGluPheCysAlaGlnGlyGlnLeuTyrgluValLeuArgAlaGlyArg----- 239
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DB 240 -----ProValThrProSerLeuValAspTrpSerMetGlyIleAlaGlyGly 256
QY 259 CTGGCTACCTGCACAAAGAAAACATCATCTTCTGTGACCTGAAGTCGGACAACTTCG 318
DB 257 MetAsnTyrluHisLeuHisLysIleIleHisArgAspLeuLysSerProAsnMetLeu 276
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QY 379 AGGCAG---TCATTCCATGAGGGCGCCCTAGGCGTGGAGGGCCTCTCGCTACAGGCC 435
DB 292 LysGluLeuSerAspLysSerThrLysMetSerPheAlaGlyThrValAlaTrpMetAla 311
QY 436 CCAGATCAGCGCTCGCATTTGATGATGAGAGGTAGATATGTTCTCTCTATGGAAAT 495
DB 312 ProGluValIleArgAsnGluProValSerGluLysValAspIleTrpSerPheGlyVal 331
QY 496 GTGTCTACAGATTGCTGTCTCAGGACAGCGCCCT----- 528
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DB 352 IleTrpGlyValGlySerAsnSerLeuHisLeu----- 362
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780	-----SerLeuSerThrPheSerSerGluAsnProSerSerAspGlyGlu	793
1699	AGGTCCCTCAAGCCTCCAGCTCCAGCAAGTCTTCCAGTGTCCTTCTCCACCC	1758
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1759	GACTCGAGAGACTCAGACATGCTACTACATACGCGCGTGTCTCGACAGTCTGAGCAT	1818
812	AsnThrAspGluArgProAspGluArgSerAspMetCysSerGlnGlySerGluIle	831
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/ Sequence 324, Application US/10153668		
/ Publication No. US20030092616A.		
/ GENERAL INFORMATION:		
/ APPLICANT: HONDA, Goichi		
/ APPLICANT: MATSUDA, Aki		
/ APPLICANT: MURAMATSU, Shuji		
/ APPLICANT: ISHIZAWA, Kenya		
/ TITLE OF INVENTION: STAT6 Activating Gene		
/ FILE REFERENCE: 1254-0207P		
/ CURRENT APPLICATION NUMBER: US/10/153,668		
/ CURRENT FILING DATE: 2002-05-24		
/ PRIOR APPLICATION NUMBER: US 60/293,172		
/ PRIOR FILING DATE: 2001-05-25		
/ PRIOR APPLICATION NUMBER: US 60/316,031		
/ PRIOR FILING DATE: 2001-08-31		
/ PRIOR APPLICATION NUMBER: US 60/328,403		
/ PRIOR FILING DATE: 2001-10-12		
/ PRIOR APPLICATION NUMBER: JP 2001-157043		
/ PRIOR FILING DATE: 2001-05-25		
/ PRIOR APPLICATION NUMBER: JP 2001-260681		
/ PRIOR FILING DATE: 2001-08-30		
/ PRIOR APPLICATION NUMBER: JP 2001-313175		
/ PRIOR FILING DATE: 2001-10-10		
/ NUMBER OF SEQ ID NOS: 488		
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/ LENGTH: 859		
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US-10-153-668-324		
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Prd. No.:		

Alignment Scores: 2.33e-10 Length: 859
pred. NO.:

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re: 295.50 Matches: 168
cent Similarity: 34.27% Conservative: 89
t Local Similarity: 22.40% Mismatches: 257
ry Match: 7.28% Indels: 236
15 Gaps: 31

39-836-392-8_COPY_22_2205 (1-2184) x US-10-153-668-324 (1-859)

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199 TCCTTTATACCCCTGGGACACATGCTACCCCAAAAATAGCTACCATCGCTCCGGC 258
207 -----ProValThrProSerLeuLeuValAspTrpSerMetGlyIleAlaGly 223
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379 AGGCAG---TCATTCATGAGGGCGCCCTAGGCGCTGGAGGCGACTCTGCTACCAAGCC 435
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GenCore version 5.1.6
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- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

lc	Score	Match	Length	DB	ID	Description
1	2184	100.0	3496	10	US-09-836-392-8	Sequence 8, Appli
2	1936.8	88.7	7015	15	US-10-132-382-5	Sequence 5, Appli
3	1936.8	88.7	7093	15	US-10-132-382-1	Sequence 1, Appli
4	1936.8	88.7	7229	15	US-10-132-382-7	Sequence 7, Appli
5	1936.8	88.7	7307	15	US-10-132-382-3	Sequence 3, Appli
6	1840	84.2	3112	13	US-10-094-749-50	Sequence 50, Appli
7	477.6	21.9	526	15	US-10-121-925-10	Sequence 10, Appli
8	64.2	2.9	1497	15	US-10-156-761-4356	Sequence 4356, Ap
9	64.2	2.9	9025608	15	US-10-156-761-1	Sequence 1, Appli
10	57.4	2.6	515	15	US-10-101-4648-149	Sequence 149, App
11	55	2.5	2218	13	US-09-820-790-1	Sequence 1, Appli
12	54.6	2.5	1825	11	US-10-16-275-321	Sequence 321, App
13	54.2	2.5	1383	11	US-09-935-464-2	Sequence 2, Appli
14	54.2	2.5	1383	15	US-10-125-835-2	Sequence 2, Appli
15	54.2	2.5	1738	11	US-09-935-464-4	Sequence 4, Appli

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Sequence 47, Appli

ALIGNMENTS

RESULT 1

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; Sequence 8, Application US/09836392
; Patent No. US20020173458A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptides,
; FILE REFERENCE: PT020P1
; CURRENT APPLICATION NUMBER: US/09/836,392
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: PCT/US00/28066
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 60/159,542
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/165,914
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/189,027
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 3496
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-836-392-8

Query Match 100.0%; Score 2184; DB 10; Length 3496;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 22 ATGCTGAGGACCTGGGCGCCACCGATGCGATGAGAACTTCTCCGAGTCCGGCAGGAG 81
OY 61 GCCAGCATGCTGCACGCGTGCAGACCCCTGATCGTGGCGCTCATCGGCATCAGCATC 120
Db 82 GCCAGCATGCTGCACGCGTGCAGACCCCTGATCGTGGCGCTCATCGGCATCAGCATC 141

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 202 GAGAACCCAGAGATCTTCCCTTTATACCCCTGGAGACATGCTCACCACCAAAATAGCC 261
 241 TACAGATCGCCTCGCGCTGCGCTTACCTGACCAAGAAACATCATCTTCTGTGACCTG 300
 262 TACAGATCGCCTCGCGCTGCGCTTACCTGACCAAGAAACATCATCTTCTGTGACCTG 321
 301 AATCGGACAAATCTGTGTGCTGCTTGTGAGCTCAAGAGACATCAACATCAAGCTA 360
 322 AATCGGACAAATCTGTGTGCTGCTTGTGAGCTCAAGAGACATCAACATCAAGCTA 381
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 382 TCTGACTTACGGGATTTGAGGACATCATTCATGAGGCGCCCTAGGCGTGGAGGCACT 441
 421 CTTGGTATCAGGCCCAAGATCAGGCTTCGATTTGATATGATGAGAGGATGATG 480
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 2062 GACACTGTGTGTGCTGACCTTTGAAATGAAACACAGAGTGGTGGTGGCGCTGTGAGG 2121
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 2161 GAGGCTTGCATCTCGCAAGAGAGG 2184
 2182 GAGGCTTGCATCTCGCAAGAGAGG 2205

GENERAL INFORMATION:

APPLICANT: WEISS, BERTRAM
 TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROLS

FILE REFERENCE: SCH-1811

CURRENT APPLICATION NUMBER: US/10/132,382

CURRENT FILING DATE: 2002-04-26

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.1

EQ ID NO 5

LENGTH: 7015

TYPE: DNA

ORGANISM: Homo sapiens

10-132-382-5

Query Match

est Local Similarity 88.7%; Score 1936.8; DB 15; Length 7015;

atches 2065; Conservative 0; Mismatches 2; Indels 117; Gaps 1;

1 ATGCTGAGGCACCTGGGGCCACCGATGTCATGAAGAACTTCCCGAGTTCGGCAGGAG 60
 4124 ATGCTGAGGCACCTGGGGCCACCGATGTCATGAAGAACTTCCCGAGTTCGGCAGGAG 4183
 61 GCCAGCATGCTGCACGCGCTGCAGCACCCCTCATCGTGGCGCTCATCGGCATCAGCATC 120
 4184 GCCAGCATGCTGCACGCGCTGCAGCACCCCTCATCGTGGCGCTCATCGGCATCAGCATC 4243
 121 CACCCGCTGCTTCCGCTTGGAGCTTGGCGGCTCAGCAGCCTCAACACACCGTGTGTCC 180
 4244 CACCCGCTGCTTCCGCTTGGAGCTTGGCGGCTCAGCAGCCTCAACACACCGTGTGTCC 4303
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 4604 TTCTCTATGGAATGTTCTACAGATTGCTGTGAGGACAGCGCCCTGCACTGGGCCAC 4663
 541 CACCACTCCAGATTGCCAAGAGCTGTCGAAGGCACTCCGCCGGTTCTGGGCGACCG 600
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 DB 5024 CTCAGGTCCAGAGATCCTCTGTGGACAGCCACCG----- 5057
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2101 GCGTGGGCGCCAGGAGTTCGCACTTTCTACCAAGTCTTACAGAGAGCTGGGCGGCGCTG 2160
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6167 GAGCGTTGCACTCGCAAGAGAAGG 6190

JLT 3
10-132-382-1
sequence 1, Application US/10132382
Publication No. US20030045699A1
GENERAL INFORMATION:
APPLICANT: WEISS, BERTRAM
TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROIDS
FILE REFERENCE: SCH-1811
CURRENT APPLICATION NUMBER: US/10/132,382
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 7093
TYPE: DNA
ORGANISM: Homo sapiens
10-132-382-1

very Match 88.7%; Score 1936.8; DB 15; Length 7093;
Fast Local Similarity 94.6%; Pred. No. 0;
Matches 2065; Conservativity 0; Mismatches 2; Indels 117; Gaps 1;
1 ATGCTGAGGCACCTGCGGGCCACCGATGCCATGAAGAACTTCTCGAGTTCGGCAGGAG 60
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4322 CACCCGCTCTGCTTCGCGCTTGAGCTCGCGCGGCTCAGCAGCCTCAACACCGTCTGCTCC 4381
181 GAGAACGCGCAGAGATTCCTCTTTATACCGCTTGGACACATGCTCACCCAAAAAATAGCC 240
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0-132-382-7
Sequence 7, Application US/10132382
Publication No. US20030045699A1
GENERAL INFORMATION:
APPLICANT: WEISS, BERTRAM
TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROLS
FILE REFERENCE: SCH-1811
CURRENT APPLICATION NUMBER: US/10/132.382
URGENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
Q ID NO 7
LENGTH: 7229
TYPE: DNA
ORGANISM: Homo sapiens
0-132-382-7

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ery Match      88.7%; Score 1936.8; DB 15; Length 7229;
st. Local Similarity 94.6%; Pred. No. 0;
tches 2065; Conservative 0; Mismatches 2; Indels 117; Gaps 1;

1  ATGCTGAGGCACCTGCGGGCCACCGCATGCATGAAGAACTTCGAGATTCCGCGCAGAG 60
4338  ATGCTGAGGCACCTGCGGGCCACCGCATGCATGAAGAACTTCGAGATTCCGCGCAGAG 4397

61  GCCAGCATGCTGACACGCGGTGTCAGACCCCTGTCATCTGTGGCCTCATCGGCATCAGCATC 120

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D5		4458	CACC CGCTCTGCTTTGCGCCCTGGAGCTCGCGCGCTCAGCAGCCTCAACACCGTGTCTGCC	4517
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D5		4518	GABAAGCGCCAGAGATTCTTCCTTTATACCCCTGGGACACATGCTCACC CCAAAAATA GCC	4577
QY		241	TACCAGATCGCCTCGGCGCTCGGCTACTGTACAAGAAAAA CATCATCTCTCTGTGACCTG	300
D5		4578	TACCAGATCGCCTCGGCGCTCGGCTACTGTACAAGAAAAA CATCATCTCTCTGTGACCTG	4637
QY		301	AGTTCGGACACATCTCGTGTGCTTGAGCTCAAGGAGCACATCAA CATCAAGCTA	360
D5		4638	AAGTCGGACACATCTCGTGTGCTTGAGCTCAAGGAGCACATCAA CATCAAGCTA	4697
QY		361	TCTGACTACGGGATTTTCGAGCGAGTCATTCCATGAGGCGCCCTAGGCGTGGAGGGCACT	420
D5		4698	TCTGACTACGGGATTTTCGAGCGAGTCATTCCATGAGGCGCCCTAGGCGTGGAGGGCACT	4757
QY		421	CCTGCTACCAAGCCCCAGAGATCAGGCTTCGATGTATATGATGAAGGTAGATG	480
D5		4758	CCTGCTACCAAGCCCCAGAGATCAGGCTTCGATGTATATGATGAAGGTAGATG	4817
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D5		4818	TTCTCCTATGAATGGTGCTCTACGAGTTGCTGT CAGCACAGCCCTGCACTGGGCCAC	4877
QY		541	CACCAGCTCCAGATTGCCAAGAGCTGTCCAAGSGCATCCGCGCCGCTTCTGGGCGACCGG	600
D5		4878	CACCAGCTCCAGATTGCCAAGAGCTGTCCAAGSGCATCCGCGCCGCTTCTGGGCGACCGG	4937
QY		601	GAGAA GTGCA NGTTCOGGOCATG CAGCGCGCTCATGTAGTAGTGCTGGGAC TAAAGCCA	660
D5		4938	GAGAA GTGCA NGTTCOGGOCATG CAGCGCGCTCATGTAGTAGTGCTGGGAC TAAAGCCA	4997
QY		661	GAGAAGCGACCGCTGGCCCTGTCCGCTGGTGAGCCAGATGAAGGACCCGACTTTTGCCACC	720
D5		4998	GAGAAGCGACCGCTGGCCCTGTCCGCTGGTGAGCCAGATGAAGGACCCGACTTTTGCCACC	5057
QY		721	TTCATGTATGAATGCTGTGCGAAGCAGACAGCGCTTCTTCTCATCCCAGGCGCAGGAG	780
D5		5058	TTCATGTATGAATGCTGTGCGAAGCAGACAGCGCTTCTTCTCATCCCAGGCGCAGGAG	5117
QY		781	TACACCGTGTGTTTTGGGATGGAAAAGAGNGATCCAGGA ACTACAGTGTGTGAACACA	840
D5		5118	TACACCGTGTGTTTTGGGATGGAAAAGAGNGATCCAGGA ACTACAGTGTGTGAACACA	5177
QY		841	GAGAAGGCGCTCATGTGAGGTGCAGAGATGTGCTGCCCTGGGATGAAGGTGAGCTGCCAG	900
D5		5178	GAGAAGGCGCTCATGTGAGGTGCAGAGATGTGCTGCCCTGGGATGAAGGTGAGCTGCCAG	5237
QY		901	CTCCAGGTCCAGAGATCCCTGTGGACGCAACCGAGGACCGAGAAA TCTACATCTACACC	960
D5		5238	CTCCAGGTCCAGAGATCCCTGTGGACGCAACCGAGGACCGAGAAA TCTACATCTACACC	5271
QY		961	CTCAAGGGCATGTGCCCTTTAACACACCCCAACAGGCGCTTGGGATCTCCAGCTGTGCTG	1020
D5		5272	-----	5271
QY		1021	ACCTGCTCTTTGGCCGTGCTGTTATTAAAAGAA TTCTACCTGTGCTTTAGCGGGCCTC	1080
D5		5272	----- AGAATTCCTACCTGTGCTTTAGCGGGCCTC -----	5300
QY		1081	CGCGATGGGCTTTGTGCTGTGTTCCCGTGTGGGGGCA CCCCA AAGGACAGCTGCTCC	1140
D5		5301	CGCGATGGGCTTTGTGCTGTGTTCCCGTGTGGGGGCA CCCCA AAGGACAGCTGCTCC	5360
QY		1141	TACCTGTGCTCACACACGCCAACAGSTCCAAGTTTCAGCATTCGCGGATGAAGACGCACCG	1200

289 TTCTGTGACCTGAAGTCGGAACAACATCTCGTGGTCCCTTGACGTCACGAGACATC 348
6 TCCGGTGAACCTGAAGTCGGAACAACATCTCGTGGTCCCTTGACGTCACGAGACATC 65
349 AACATCAAGCTATCTGACTACGGAATTCAGGACGATTCATCCATGAGGCGCCCTAGGC 408
66 AACATCAAGCTATCTGACTACGGAATTCAGGACGATTCATCCATGAGGCGCCCTAGGC 125
409 GTGAGGCGCTCTCTGCTACGAGGCGCCAGAGATCAGGCTCGCATTTATATGATGAG 468
126 GTGAGGCGCTCTCTGCTACGAGGCGCCAGAGATCAGGCTCGCATTTATATGATGAG 185
469 AAGTAGATATGTTCTCTATGGAATGGTCTCTACGAGTTGCTGTCAGGACAGCGCCCT 528
186 AAGTAGATATGTTCTCTATGGAATGGTCTCTACGAGTTGCTGTCAGGACAGCGCCCT 245
529 GCATGAGGCGCTCTCTGCTACGAGGCGCCAGAGATCAGGCTCGCATTTATATGATGAG 588
246 GCATGAGGCGCTCTCTGCTACGAGGCGCCAGAGATCAGGCTCGCATTTATATGATGAG 305
589 CTGAGGCGCTCTCTGCTACGAGGCGCCAGAGATCAGGCTCGCATTTATATGATGAG 648
306 CTGAGGCGCTCTCTGCTACGAGGCGCCAGAGATCAGGCTCGCATTTATATGATGAG 365
649 GACATCAAGCGAG 707
366 GACATCAAGCGAG 425
708 GACTTTGCGCAGCTCTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 766
426 GACTTTGCGCAGCTCTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 485
767 CCAGGCGCAGGAGTACACCGT-GGTGTTTGGGATGGAAA 806
486 NCCAGGCGCAGGAGTACACTGTGGGTGTTTGGGATGGAAA 526

LT 8

10-156-761-4356
Sequence 4356, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
PRIORITY FILING DATE: 2002-05-29
PRIORITY FILING DATE: 2001-05-29
PRIORITY FILING DATE: 2001-05-30
PRIORITY FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109

Q ID NO 4356
LENGTH: 1497
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1497)
0-156-761-4356

ery Watch 2.9%; Score 64.2; DB 15; Length 1497;
st Local Similarity 43.4%; Pred No. 1.1e-07;
tches 294; Conservative 0; Mismatches 383; Indels 0; Gaps 0;
23 CCGATGCCATGAAGAATCTCCGAGTTCCGGCAGAGAGCCAGCATGCTGCAGCGCTGC 82

164 CCAGGAGCCCGGTCTCCAAAGGCCCGCTTCAACGCGGAGGCCCGAGTCGGTGGCGGCTCA 223
83 AGCACCCCTGCTATCGTGGCGCTCATCGGCATCAGCATCCACCGCTCTGCTTCGGCCTGG 142
224 ACACCATCGGTCTGTCGGGTGTAGGACTCCGGGAGAGACGTCGTCGGGCACTCCACCG 283
143 AGTCGCGCGCTCAGCAGCCTCAACACCGTCTCTCCGAGAACGCCAGAGATTCTTCT 202
284 TCCGCTACATCGTGTGAGCTGGTCGAGGGCGCACCATCCGCGACCTGCTGTGTCACAG 343
203 TTATACCCCTGGGACACATGCTCACCCAAAATAGCTACAGATCCGCTCGGCGCTGG 262
344 CGAGGCCCGGGCCCGAGCAGGGTTCATCGTCTCCGGGTGCTGGAGGCGCTGG 403
263 CTACCTGCACAAAGAAACATCATCTTCTGTGACCTCAAGTCGGACAACTTCTGTGT 322
404 CTTACTCGCACAGCAGCATCTGTGACCGCGCATCAAGCGGCAACGTCATCATCA 463
323 GGTCCCTTACCTCAGGAGCAGCATCAACATCAAGCTATCTGACTACGGGATTTGGAGGC 382
464 CGACAAACGCTGCCGTGAAGTTCATGACCTTCGGCATCGCGCGGCTTCACACGCGCGC 523
383 AGTCATTCATCAGGCGCGCTTAGCGGTGGAGGCGCATCTCTGGTACCGAGGCCAGAGA 442
524 AGTCGAGATGAGCAGACCGCATGTCATGGGACCGCGCATCTGTTCGCCCGAGC 583
443 TCAGGCTCGCATTTCTATATGATGAGAGAGTAGATATTTCTCTATGGAATGGTGTCT 502
584 AGCGCTCGGAAAGCGGTTCGACACCGCAGCGACCTGTACCGACCGTTGCTGTCT 643
503 ACGAGTTGCTGTCAGGACAGCGCTTCGCTGCGGCGCCAGCCAGCTCCAGTCCAGTCCCAAGA 562
644 ACGAACTCTCGCTCGCGCGCGCTTTCACCGTGAGACCGCGCTCTCCGTGTCTTACC 703
563 AGCTGTCAAGGCGCATCCGCGCGCTTCTGGGCGAGCGGAGAGTGCAGTCCGCGGAC 622
704 AGCAGTGCAGACATCCGCTGCCCGCTCCGAGTCCGGAAGGGCGCGCGGAGC 763
623 TCGAGGCGCTCATGTCAGTGTGCGGACACTAAGCCAGAGAGCGACCGCTGCGCCTGT 682
764 TCGAGGACTCGTGTGATGCTGCTCGGAGGATCCCGACGACCGGTTCCAGACCGCG 823
683 CGTGGTGCAGCAGATG 699
824 AGGAGATCGCGGCGTG 840

RESULT 9

US-10-156-761-1
Sequence 1, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
PRIORITY FILING DATE: 2002-05-29
PRIORITY FILING DATE: 2001-05-29
PRIORITY FILING DATE: 2001-05-30
PRIORITY FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1
LENGTH: 9025608
TYPE: DNA
ORGANISM: Streptomyces avermitilis

FEATURE:

NAME/KEY: misc feature
 LOCATION: (4187715)
 OTHER INFORMATION: a, t, c, g, other or unknown
 10-156-761-1

Query Match 2.9%; Score 64.2; DB 15; Length 9025608;
 est Local Similarity 43.4%; Pred. No. 1.4e-06;
 Matches 294; Conservative 0; Mismatches 383; Indels 0; Gaps 0;

23 CCGATGCGCATGAAGAACTTCTCCGAGTTCCGGCAGGAGCCAGCATGTCGACGGGCTGC 82
 5351896 CCGAGGACCGGTCTCCAGGCGCGCTTACGGCGGAGGCCAGTCGGTGGCGGGCTCA 5351955

83 AGACCCCTCGATCGTGGCGCTCATCGGCATAGCATCCACCGCTCTGCTTCGCGCTGG 142
 5351956 ACCACCATCGGTGCTGCGCGTGTAGCACTCCGGCAGGACGTCGTCGGGCACTCCACG 5352015

143 AGCTCGCGCGCTCAGCAGGCTCAACACCGTGTGTCGAGAACCCAGAGATTCTTCT 202
 5352016 TCCGTATCATCGTATGGAGCTGTCGAGGCGCGACATCCCGGACCTGCTGCTCAACG 5352075

203 TTATACCCCTGGGACATGCTCACCACCAAAATAGCTTACAGATCGCTCGGGCTGG 262
 5352076 CCGAGGCGCGCGGCGCGAGCGGCTGATCATGCTCTCGGGTGTGTCGAGGCGCTGG 5352135

263 CCTACCTGTCACAGAAACATCATCTTCTGTGACCTGAAGTCGAGCAACATCTGGTGT 322
 5352136 CCTACTCGCACAGCAGGATGTCGACCGGACATCAAGCCGCGCAACGTCATCA 5352195

323 GGTCCCTTACGTCACAGGAGCACAATCAACATCAAGCTATCTGACTACGGGATTTGAGGC 382
 5352196 CGCACACGGTGCCTGAAGTCTATGACTTCGGCATCGCGCGCCCTCGACGGCGCG 5352255

383 AGTCATTCCATGAGGGCGCTTAGGCGTGGAGGCACTCTGGCTTACAGGCCCGCAGAGA 442
 5352256 AGTCGAGATGACGCGAGACCGGATGTCATGGCAGCGCGAGTACCTGTCGCGCGAGC 5352315

443 TCAGGCTCGCATTTATATGATGAGAAGGTAGATATGTCCTCATGGAATGTCCT 502
 5352316 AGGCGTCTCGAAGGCGGTGCGACCCAGCGAGCTGTACCGGACCGGTTCCTGCTCT 5352375

503 ACAGATGCTGTGACAGACAGCGCTGACCTGGGCAACACAGCTCCAGATTGCCAAGA 562
 5352376 ACAGATCTCTCGCGCTGCGGCGCGCGCTTACCGCGTGAGACCCGCTGCTGCTTACC 5352435

563 AGCTGTCACAGGSCATCCCGGCTTCTGGGCGACCGGAGAGTGCAGTTCGGCGAC 622
 5352436 AGCAGTGCAGGACATCCCGGTGCGCGCTCCGAGGTCCGGAAGGGCGCGCGCGAGC 5352495

623 TGCAGGCGCTCATGATGAGTGTGCGACACTAAGCCAGAGAGCGACCGTGGCCCTGT 682
 5352496 TGCAGGACCTGATGATGCTGCTGCGAAGGATCCCGACGCGGTTCCAGACCGCG 5352555

683 CGGTGCTGACCCAGATG 699
 5352556 AGGAGATGCGCGGCTG 5352572

JLT 10

10-101-464A-149
 Sequence 149, Application US/10101464A
 Publication No. US20030046728A1
 GENERAL INFORMATION:
 APPLICANT: Strabala, Timothy
 APPLICANT: Nieuwenhuizen, Nicolaas
 APPLICANT: Higgins, Colleen M.
 TITLE OF INVENTION: Compositions Isolated from Plant Cells
 TITLE OF INVENTION: and their Use in the Modification of Plant Cell Signaling
 FILE REFERENCE: 11000.1020C2
 CURRENT APPLICATION NUMBER: US/10/101,464A
 CURRENT FILING DATE: 2002-03-18
 PRIOR APPLICATION NUMBER: 09/704,302

PRIOR FILING DATE: 2000-11-01
 PRIOR APPLICATION NUMBER: 09/228,986
 PRIOR FILING DATE: 1999-01-12
 PRIOR APPLICATION NUMBER: 60/162,866
 PRIOR FILING DATE: 1999-11-01
 PRIOR APPLICATION NUMBER: PCT/US00/00724
 PRIOR FILING DATE: 2000-01-11
 NUMBER OF SEQ ID NOS: 989
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 149
 LENGTH: 515
 TYPE: DNA
 ORGANISM: Eucalyptus grandis
 US-101-464A-149

Query Match 2.6%; Score 57.4; DB 15; Length 515;
 Best Local Similarity 51.8%; Pred. No. 7e-06;
 Matches 130; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 273 CAAGAAAACATCATCTTCTGTGACCTGAGTCGAGCAACATCTGTGTGGTCCCTTGA 332
 DB 58 CAAGCAGACCATATTATACACCGCGACATGAGACCAACCATCTGCTCGACGAGAAGTG 117

QY 333 CQTCAAGGAGCACAATCAACATCAAGTATCTGACTACGGGATTTTCGAGGCGAGTCATTCCA 392
 DB 118 GGTTCGCAAGGTGTCGGAATTCGGGCTCTCGAAGTTCGGCCGACGTCGGTGTCCAAGGC 177

QY 393 TGAGGCGCGCTTAGCGGTGAGGCGACTCTCTGGTACAGGCCCGCCAGAGATCAGGCGCTCG 452
 DB 178 CCACGTCAGCACCGGTGTAAGGCGACCTTCGGGTACTCTGGATCCAGAGTACTACAGCG 237

QY 453 CATTTATATGATGAGAAGTAGATATGTTCTCTATGATGATGCTCTACGAGTTGCT 512
 DB 238 CCAGCAGTGAAGTCAAGTCCGACGCTGCTCTCTCGGGTGTGCTATTTCGAGGTGCT 297

QY 513 GTCAGACAGC 523
 DB 298 GTGTCAAGGC 308

RESULT 11

US-09-820-790-1
 Sequence 1, Application US/09820790
 Publication No. US20030140354A1
 GENERAL INFORMATION:
 APPLICANT: SHAO, Wei et al.
 TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 TITLE OF INVENTION: THEREOF
 FILE REFERENCE: CL001204
 CURRENT APPLICATION NUMBER: US/09/820,790
 CURRENT FILING DATE: 2001-03-30
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 2218
 TYPE: DNA
 ORGANISM: Human
 US-09-820-790-1

Query Match 2.5%; Score 55; DB 13; Length 2218;
 Best Local Similarity 48.0%; Pred. No. 5.1e-05;
 Matches 157; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 240 CTACAGATCGCTCGGCGCTTACCTGCAAGAAAAACATCATCTTCTGTGACCT 299
 DB 612 CCAGCAGATCTCGAGCGCTTCTCCATTGTCACCAATGGGGTCTCCACAGACCT 671

QY 300 GAAGTCGAGCAACATCTTGTGTGGTCCCTTGTGAGCTCAAGAGCAGATCAACATCAAGCT 359
 DB 672 CAAGCCGAGAACCTGCTTCTGCGCAGCAAGTCAAGGGGCTGCACTGAAGCTGGCAGA 731

QY 360 ATCTGACTACGGGATTTTCGAGGCGAGTCATTCATGAGGCGCCCTAGGCGTGGAGGCGAC 419

732 CTTCGGCTAGCTATCGAGGTGACGGGGACACGAGGCATGGTTTGGTTGCTGGCCAC 791
420 TCTCGCTACAGGCCCCAGAGATCAGCCCTCGCATGTATATGATGAGAGGTAGATAT 479
792 ACCAGCTACCTGTCCCTCGAGTCTTCGAAAGAGCGGTATGGCAAGCTGTGGACAT 851
480 GTTCTCCTATGAAATGGTGCTCTACAGTTCGTCTCAGGACAGCGCCCTGCACCTGGGCCA 539
852 CTGGGATGTTGGGGTGATCTGTACATCTCTGTGGCTACCCACCTCTCTGGGACGA 911
540 CCACAGCTCCAGATGCCAAAGCT 566
912 GGACAGCACAAGCTGTACCAGCAT 938

LT 12
0-116-275-321
Sequence 321, Application US/10116275
Publication No. US20030211476A1
GENERAL INFORMATION:
APPLICANT: Elan Pharmaceutical Technology
APPLICANT: O'Mahony, Daniel J.
APPLICANT: Brayden, David
APPLICANT: Byrne, Daragh
APPLICANT: Lambkin, Imelda
APPLICANT: Higgins, Lisa
TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
FILE REFERENCE: E1067/20087
CURRENT APPLICATION NUMBER: US/10-116,275
PRIORITY FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SOFTWARE: Patent in version 3.1
SEQ ID NO 321
LENGTH: 1825
TYPE: DNA
ORGANISM: Homo sapiens
0-116-275-321

Query Match 2.5%; Score 54.6; DB 13; Length 1825;
Best Local Similarity 47.7%; Pred. No. 6.2e-05;
Matches 156; Conservative 1; Mismatches 170; Indels 0; Gaps 0;

240 CTACAGATCGCTCGGGCTGGCTACCTGACAGCAAGAAACATCATCTTCTGTGACCT 299
397 CAGCAGATCTGTGAGGCGCTTCTCATTTGTCCAAATGGGGTGTCCACAGACCT 456
300 GAAGTCGACAAATCTGGTGTGGTCTTGAAGTCAAGGACACATCAACATCAAGCT 359
457 CAAGCCGAGAACCTGCTTCTGCGCAGCAAGTGCAAGGGGCTGCAGTGAAGCTGGCAGA 516
360 ATCTGACTACGGGATTCAGGAGCTATTCATGAGGGCGCCCTAGCGTGGAGGCAC 419
517 CTTCGGCTAGCTATGAGGTGCAGGGGACACGAGGCATGGTTGGTTTGGCTGGCAC 576
420 TCTGTCTACCGGCCCCAGAGATCAGGCTCGCATTTATATGATGAGAGGTAGATAT 479
577 ACCAGCTACCTGTCCCTGAGTCTTCGCAAGAGCGGTACGCGAGCCGCTGGACAT 636
480 GTTCTCCTATGAAATGGTGCTCTACAGTTCGTCTCAGGACAGCGCCCTGCACCTGGGCCA 539
637 CTGGGATGTTGGGGTGATCTGTACATCTCTGTGGCTACCCACCTCTCTGGGACGA 696
540 CCACAGCTCCAGATGCCAAAGCT 566
697 GGACAGCACAAGCTGTACCAGCAT 723

LT 13
09-935-464-2
Sequence 2, Application US/09935464
Publication No. US2003027153A1

GENERAL INFORMATION:
APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Parker, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHI
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/1H702 US1
CURRENT APPLICATION NUMBER: US/09/935,464
PRIORITY FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patent in version 3.0
SEQ ID NO 2
LENGTH: 1383
TYPE: DNA
ORGANISM: Homo sapiens
US-09-935-464-2

Query Match 2.5%; Score 54.2; DB 11; Length 1383;
Best Local Similarity 49.9%; Pred. No. 7.4e-05;
Matches 168; Conservative 0; Mismatches 163; Indels 6; Gaps 1;
QY 240 CTACAGATCGCTCGGGCTGGCTACCTGACAGCAAGAAACATCATCTTCTGTGACCT 299
DB 372 CAGCAGCTTGTTCGCGAGTGAATACCTACATGAGATGGCATGTCCACAGACAT 431
QY 300 GAAGTCGACAAATCTGGTGTGGTCCCTTGACGTCAAGGACACATCAACATCAAGCT 359
DB 432 AAAGCCGAGAACCTGCTCTTACCTTACCTTGAAGAGAACTCTAAGATCATGAT 485
QY 360 ATCTGACTACGGGATTTTCGAGGAGTCAATTCCTAGGGGCGCCCTAGGCTGGAGGCAC 419
DB 486 CACTGACTTGTCTGTCCAGATGGAACAGATGGCATGTCTCACTGCTGTGGAC 545
QY 420 TCTGTCTACCGGCCCCAGAGATCAGGCTCGCATTTATATGATGAGAGGTAGATAT 479
DB 546 CCCAGCTACGTGGCTCCAGAGTGTGGGCCAGAACCTTACAGCAAGCTGTGGATTG 605
QY 480 GTTCTCCTATGAAATGGTGCTCTACAGTTCGTCTCAGGACAGCGCCCTGCACCTGGGCCA 539
DB 606 CTGGTCCATCGCGCTCATCACTACATTTGCTCTGTGGATACCCCCCATTTCTATGAAGA 665
QY 540 CCACAGCTCCAGATGCCAAAGCTGTCCAAAGGGC 576
DB 666 AACGAGTCTAAGCTTTTCGAGAGATCAAGAGGGC 702

RESULT 14
US-10-125-835-2
Sequence 2, Application US/10125835
Publication No. US20030092019A1
GENERAL INFORMATION:
APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Parker, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING
TITLE OF INVENTION: NEUROPSYCHIATRIC
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/0H702 US0
CURRENT APPLICATION NUMBER: US/10/125,835
PRIORITY FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US/09/757,300
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patent in version 3.0
SEQ ID NO 2
LENGTH: 1383
TYPE: DNA
ORGANISM: Homo sapiens
US-10-125-835-2

Query Match 2.5%; Score 54.2; DB 15; Length 1383;

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est Local Similarity 49.9%; Pred. No. 7.4e-05;
atches 168; Conservative 0; Mismatches 163; Indels 6; Gaps 1;

240 CTACAGATCGCCTCGGCGCTACCTGACAGAAACATCATCTTCTGTGACCT 299
372 CCAGCAGGCTTTGTCGCGAGTGAATACCTATGAGAAATGGCATCGTCCACAGAGACTT 431
300 GAAGTCGACAAACATCTGTGTGTGTCCTTACGCTGACGAGCAGACATCAACATCAAGCT 359
432 AAAGCCGAAACCTGCT-----TTACCTTACCCCTGAAGAGAACTCTAAGATCATGAT 485
360 ATCTGACTACGGGATTTGAGGAGTCACTTCATGAGGCGCCCTAGGCTGGAGGGCAC 419
486 CACTGACTTTGGTCTGTGCAAGATGGAACAGATGGCATCATGTCCACTGCTGTGGGAC 545
420 TCTGGCTACAGGCCCCAGAGATCAGGCTCGCATTTGATGATGAGAGGCTAGATAT 479
546 CCAGGCTAGTGGCTCCAGAGTGTGCGCCAGAAACCTACAGCAGGCTGTGGATTG 605
480 GTTCTCCTATGGAATGGTGTCTACAGTGTGTGTCAGACAGCGCCCTGCACTGGGCCA 539
606 CTGCTCCATCGGGCTCATACCTACATATTGCTCTGTGATACCCCCCATTTCTATGAAGA 665
540 CCACCAGCTCCAGATGCCAAGAGCTGTCCAGGGC 576
666 AACGAGCTTAAGCTTTTCGAGAAGATCAAGGAGGC 702

ULT 15
09-935-464-4
sequence 4, Application US/09935464
ublication No. US20030027153A1
GENERAL INFORMATION:
APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Parker, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIA
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/1H702 US1
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT FILING DATE: 2001-08-23
PRIOR FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 1738
TYPE: DNA
ORGANISM: Hmo sapiens
09-935-464-4

nary Match 2.5%; Score 54.2; DB 11; Length 1738;
est Local Similarity 49.9%; Pred. No. 7.9e-05;
atches 168; Conservative 0; Mismatches 163; Indels 6; Gaps 1;

240 CTACAGATCGCCTCGGCGCTACCTGACAGAAACATCATCTTCTGTGACCT 299
389 CCAGCAGGCTTTGTCGCGAGTGAATACCTACATGAGATGGCATCGTCCACAGAGACTT 448
300 GAAGTCGACAAACATCTGTGTGTGTCCTTACGCTGACGAGCAGACATCAACATCAAGCT 359
449 AAAGCCGAAACCTGCT-----TTACCTTACCCCTGAAGAGAACTCTAAGATCATGAT 502
360 ATCTGACTACGGGATTTGAGGAGTCACTTCATGAGGCGCCCTAGGCTGGAGGGCAC 419
503 CACTGACTTTGGTCTGTGCAAGATGGAACAGATGGCATCATGTCCACTGCCCTGTGGGAC 562
420 TCTGGCTACAGGCCCCAGAGATCAGGCTCGCATTTGATGATGAGAGGTAGATAT 479
563 CCCAGGCTACGTGGCTCCAGAAAGTGTGGCCAGAAACCCCTACAGCAGGCTGTGGATTG 622
480 GTTCTCCTATGGAATGGTGTCTACGAGTTGCTGTACGAGCAGCGCCCTGCACTGGGCCA 539

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Db 623 CTGGTCCATCGGCGCTCATCACTACATATTCGCTCTGTGGATACCCCCCATTTCTATGAAGA 682
QY 540 CCACCAGCTCCAGATTGCCAAGAAAGCTGTCCAAGGGC 576
Db 683 AACGGAGCTTAAGCTTTTCGAGAAGATCAAGGAGGC 719

Search completed: December 14, 2003, 06:55:23
Job time : 7:10 secs

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